



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 164100

**TO: Patricia Duffy**  
**Location: REM-3B05/3C18**  
**Art Unit: 1645**  
**Saturday, September 03, 2005**

**Case Serial Number: 09/616247**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

### Search Notes

Examiner Duffy,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524

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STIC-Biotech/ChemLib

164100

From: Duffy, Patricia  
Sent: Saturday, August 27, 2005 2:10 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

IN RE: 09/616,247

Please search the amino acids sequence of SEQ ID NO:4.

Please run the amino acid sequence of SEQ ID NO:4 against the NA database.

Please include a commercial and interference database search.

Please print out top 100 hits.

Patricia A. Duffy, Ph.D.

Art Unit 1645

Remsen 3B05; Mailbox 3C18

571-272-0855

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:47:12 ; Search time 164 Seconds

(without alignment)  
35.374 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	2	AAW25795 Peptide d
2	81	100.0	15	3	AAW79543 E. coli d
3	81	100.0	15	4	AAW9341 Vaccine r
4	81	100.0	15	5	AAU09842 E.coli dn
5	81	100.0	15	5	AAU98876 E. coli D
6	81	100.0	15	5	AAE19457 Human hea
7	81	100.0	15	6	ABR55132 E. coli d
8	81	100.0	16	4	AAW99344 Vaccine r
9	81	100.0	16	5	AAU98852 E.Coli DN
10	81	100.0	16	6	ABR55126 E. coli d
11	81	100.0	118	4	AAU02075 Synthetic
12	81	100.0	131	3	AAH11396 E. coli e
13	81	100.0	131	4	AAW74197 OmpA-J do
14	81	100.0	131	4	AAW70767 Expressio
15	81	100.0	131	4	AAW72018 E. coli O
16	81	100.0	340	4	AAU17588 Novel sig
17	81	100.0	340	7	ADB94296 Human nov
18	81	100.0	341	4	AAU17587 Novel sig
19	81	100.0	341	7	ADB94295 Human nov
20	81	100.0	373	6	ABM67485 Photorhab
21	81	100.0	376	8	ADR89339 E. coli p
22	81	100.0	376	8	ADR18036 Bacterial
23	81	100.0	378	8	ADN17733 Bacterial
24	81	100.0	378	8	ADS42875 Bacterial
25	81	100.0	380	7	ADF05627 Bacterial

26	81	100.0	380	7	ABOG2494	Abog2494 Klebsiell
27	81	100.0	399	3	AAH11395	E. coli e
28	81	100.0	399	4	AAW74196	OmpA-DnaJ
29	81	100.0	399	4	AAW70766	Expressio
30	81	100.0	399	4	AAW72017	E. coli O
31	81	100.0	459	4	AAU02077	Synthetic
32	81	100.0	476	4	ABG17771	Novel hum
33	74	91.4	365	8	ADS21615	Bacterial
34	73	90.1	344	6	ABP80877	N. gonorr
35	73	90.1	376	8	ADS23054	Bacterial
36	72	88.9	15	2	AAW95446	RA suscep
37	72	88.9	15	2	AAW25796	Peptide d
38	72	88.9	15	5	AAE19458	Heat shoc
39	72	88.9	15	6	ABR55133	E. coli d
40	69	85.2	382	8	ADN25412	Bacterial
41	69	85.2	384	8	ADS43419	Bacterial
42	67	82.7	376	8	ADR31368	Stress re
43	67	82.7	379	8	ADN24677	Bacterial
44	67	82.7	380	8	ADN21920	Bacterial
45	64.5	79.6	14	2	AAW95445	RA suscep
46	63	77.8	376	8	ADN17394	Bacterial
47	63	77.8	389	8	ADO25512	E-faecali
48	63	77.8	389	8	ADO25510	E-faecali
49	62	76.5	374	8	ADS24625	Bacterial
50	62	76.5	381	7	ABO78428	Pseudomon
51	61	75.3	378	8	ADN25797	Bacterial
52	61	75.3	385	6	ADB10662	Alloiooc
53	60	74.1	375	8	ADS26826	Bacterial
54	60	74.1	376	8	ADS26454	Bacterial
55	59	72.8	358	8	ADN26988	Bacterial
56	58	71.6	332	3	AAW14804	Arabidops
57	58	71.6	367	3	AAW14803	Arabidops
58	58	71.6	379	5	ABR55579	Lactococc
59	58	71.6	379	8	ADS29490	Bacterial
60	58	71.6	385	8	ADS27721	Bacterial
61	58	71.6	456	3	AAW14802	Arabidops
62	57	70.4	369	8	ADS30613	Bacterial
63	57	70.4	377	5	ABR48799	Listeria
64	56	69.1	352	2	AAW22358	S. pneumo
65	56	69.1	362	8	ADN26652	Bacterial
66	56	69.1	378	6	ABU00882	S. pneumo
67	56	69.1	378	6	ABP81556	Streptoco
68	56	69.1	378	8	ADK48132	Streptoco
69	56	69.1	379	5	ADP28852	Streptoco
70	56	69.1	379	5	ADR94852	Novel S.
71	56	69.1	396	5	ABP28853	Streptoco
72	56	69.1	407	8	ADL05213	M. catarr
73	55	67.9	368	3	AAW05934	Protein d
74	54	66.7	15	2	AAW25798	Peptide d
75	54	66.7	15	6	ABR55123	E. coli d
76	54	66.7	332	3	AAW48466	Arabidops
77	54	66.7	367	3	AAW48465	Arabidops
78	54	66.7	383	2	AAW34469	Porphorym
79	54	66.7	384	2	AAW34345	Arabidops
80	54	66.7	456	3	AAW48464	Arabidops
81	52	64.2	360	8	ADS21338	Bacterial
82	52	64.2	372	6	ADK44776	Bacterial
83	52	64.2	375	6	ADK33697	Acinetoba
84	52	64.2	376	8	ADN18559	Bacterial
85	50	61.7	297	6	ABU26627	Protein e
86	50	61.7	320	3	AAW30655	Arabidops
87	50	61.7	348	3	ABW30654	Arabidops
88	50	61.7	379	6	ABW70982	Staphyloc
89	49	60.5	295	3	AAW53768	Arabidops
90	49	60.5	295	3	AAW53767	Arabidops
91	49	60.5	323	3	AAW53766	Arabidops
92	49	60.5	323	3	AAW53765	Arabidops
93	49	60.5	350	3	AAW53764	Arabidops
94	49	60.5	350	3	AAW53763	Arabidops
95	49	60.5	370	8	ADK28176	Bacterial
96	48	59.3	423	8	ADS23586	Bacterial
97	47	58.0	284	3	AAW50787	Arabidops
98	47	58.0	292	3	AAW16068	Arabidops

99 47 58.0 309 3 AAG16067 Aag16067 Arabidops  
100 47 58.0 337 3 AAG16066 Aag16066 Arabidops

## ALIGNMENTS

RESULT 1  
AAW25795  
ID AAW25795 standard; peptide; 15 AA.

XX AC AAW25795;

XX XX 06-APR-1998 (first entry)

XX Peptide dnaJp1 which protects against arthritogenic peptides.

XX dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;  
KW arthritogenic peptide; autoimmune disease; systemic immune system;  
KW anti-dnaJp1 antibody; passive immunisation;  
KW rheumatoid arthritis-susceptibility detection.

XX OS Escherichia coli.

XX XX WO9734002-AL.

XX PD 18-SEP-1997.

XX PF 20-FEB-1997; 97WO-US002957.

XX PR 15-MAR-1996; 96US-00618464.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Carson DA, Albani S;

XX XX WPI; 1997-470892/43.

XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1  
PT - also determining pre-disposition to rheumatoid arthritis by detecting  
PT anti-arthritogenic peptide antibodies.

XX PS Disclosure; Page 5; 44pp; English.

XX Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from  
CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce  
CC relatively strong immune response in seropositive adult rheumatoid  
CC arthritis patients. This peptide was used in a vaccine for protecting  
CC against arthritogenic peptides. The vaccine contains a carrier, pure  
CC dnaJp1 peptide or a recombinant gene expression vector encoding the  
CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or  
CC other autoimmune diseases). Vaccines can target the arthritogenic  
CC peptides before they are presented to the systemic immune system. Anti-  
CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies  
CC can be used to detect rheumatoid arthritis-susceptibility sequences on  
CC HLA or in populations of E. coli in the gastrointestinal tract

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
Db 1 QKRAAYDQYGHAAFE 15

RESULT 2  
AAAY79543  
ID AAY79543 standard; peptide; 15 AA.  
XX XX AAY79543;  
AC

XX 15-AUG-2000 (first entry)  
XX E. coli dnaJp1 heat shock protein peptide.  
XX Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator;  
KW autoimmune disease; allergy; cancer; infection; graft rejection;  
KW immunotherapy; therapy; major histocompatibility complex; MHC; dnaJp1;  
KW heat shock protein.  
XX OS Escherichia coli.  
XX XX WO200023053-A2.  
XX PD 27-APR-2000.  
XX PF 19-OCT-1999; 99WO-US024666.  
XX PR 20-OCT-1998; 98US-0105018P.  
XX PA (ALBA/) ALBANI S.  
XX PI Albani S;  
XX XX WPI; 2000-339492/29.  
XX New artificial antigen presenting cells useful for isolating and  
PT expanding T cells, and modulating T cell responses for the treatment of  
PT e.g. autoimmune diseases, allergies.  
XX PS Disclosure; Page 42; 179pp; English.  
XX This peptide is derived from Escherichia coli heat shock protein dnaJp1.  
CC Novel artificial antigen presenting cells (APC) of the invention comprise  
CC antigens, such as the present peptide, that are presented by a major  
CC histocompatibility complex (MHC) component for contact with, and  
CC recognition by, a T cell receptor. The invention is directed to  
CC artificial APC and methods of making APC, which are used to isolate and  
CC expand T cell populations and to modulate T cell responses. The invention  
CC also provides novel methods for the identification and isolation and  
CC antigen-specific T cells. The methods provide for the construction of  
CC liposomes containing MHC:peptide complexes, accessory molecules, co-  
CC stimulatory molecules, adhesion molecules, and other molecules irrelevant  
CC to T cell binding or modulation that are used in the binding of  
CC artificial APC to solid support systems that may be used in the retrieval  
CC and identification and antigen-specific T cells. Devices and methods are  
CC provided for treating conditions that would benefit from modulation of T  
CC cell response, e.g. autoimmune disorders (especially type I diabetes  
CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis,  
CC juvenile rheumatoid arthritis and uveitis), allergies, cancer, viral  
CC infections, and graft rejection  
XX SQ Sequence 15 AA;  
Query Match 100.0%; Score 81; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 1 QKRAAYDQYGHAAFE 15  
RESULT 3  
AAAM99341  
ID AAAM99341 standard; peptide; 15 AA.  
XX AC AAAM99341;  
XX XX 07-DEC-2001 (first entry)  
XX DE Vaccine related MHC ligand peptide SEQ ID NO:444.  
XX

Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.

OS Homo sapiens.

XX WO200170772-A2.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-FR000872.

XX 23-MAR-2000; 2000FR-00003711.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;

XX WPI; 2001-611470/70.

XX Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.

XX Claim 9; Page 107; 149pp; French.

XX The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodulator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cycostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also where (I) is a MHC ligand (Ia) in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

RESULT 4

AAU09842  
ID AAU09842 standard; peptide; 15 AA.

XX AAU09842;

XX 26-FEB-2002 (first entry)

XX E.coli dnaJp1 heat shock protein-derived peptide.

XX

Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic; dermatological; immunosuppressive; ophthalmological; antiallergic; cytostatic; virucidal; antibacterial; artificial antigen presenting cell; liposome; major histocompatibility complex; MHC; T cell; allograft; cytokine production; T-helper 2 response; transplantation therapy; autoimmune disease; type 1 diabetes mellitus; multiple sclerosis; rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis; uveitis; allergy; cancer; infection; dnaJp1 heat shock protein.

XX Escherichia coli.

XX WO200180833-A1.

XX 01-NOV-2001.

XX 20-APR-2000; 2000WO-IT000161.

XX 20-APR-2000; 2000WO-IT000161.

XX (ALBA/) ALBANI S.

XX Albani S;

XX WPI; 2002-055316/07.

XX New artificial antigen presenting cell, useful for modulating T cell response for treating allergies and cancers, comprises liposome, major histocompatibility complex, antigen and accessory molecule components.

XX Disclosure; Page 46; 195pp; English.

XX The invention relates to an artificial antigen presenting cell (I) comprising liposome, major histocompatibility complex (MHC), antigen and accessory molecule components. (I) is used in methods for the following: (1) identifying T cells specific for an antigen of interest; (2) isolating T cells specific for an antigen of interest; (3) modulating T cell response; (4) characterising the functional state of antigen-specific T cells; (5) treating a condition in a subject which would be benefited by altering the functional pattern of cytokine production by certain antigen-specific T cells to increase T-helper (Th) 2 response and/or decrease Th1 response; (6) identifying antigen-specific T cells specific for epitopes on a graft donor's tissue likely to elicit graft versus host rejection response; and (7) treating a recipient mammal to reduce rejection of allografts in a transplantation therapy regime.

XX Method (5) is useful for treating autoimmune disease such as type 1 diabetes mellitus, multiple sclerosis, rheumatoid arthritis, CC dermatomyositis, juvenile rheumatoid arthritis or uveitis. Alternatively it is useful for treating allergy due to allergens such as dust, animal skin bypass products, vegetables, fruits, pollen or chemicals, cancer, viral infection, bacterial infection. Addition of the accessory CC molecules, as well as co-stimulatory molecules, and other proteins in CC proper orientation in the liposomes allow for substantially improved CC binding association and manipulation of T cells which is very important CC in the identification and stimulation of antigen-specific T cells. The CC present sequence represents E.coli dnaJp1 heat shock protein-derived CC peptide used in the method of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

AAU98876

ID AAU98876 standard; peptide; 15 AA.

XX

AAU98876;

XX	22-AUG-2002 (first entry)	
DT	E. coli DNAJ PI immunogenic peptide.	
DE		
XX		
XX	Immunogenic peptide; heat shock protein; HSP; DNAB; immunomodulatory;	
KW	Cytostatic; antiinflammatory; antibacterial; antiarthritis; human;	
KW	autoimmune disease; arthritis; articular juvenile idiopathic arthritis;	
KW	infectious disease; inflammatory bowel disease; cancer; HDJ2;	
KW	mucosal toleration; DNA vaccination; energy induction.	
XX		
OS	Escherichia coli.	
XX		
PN	WO200236611-A2.	
PD	10-MAY-2002.	
XX		
PF	31-OCT-2001; 2001WO-US045344.	
XX		
PR	01-NOV-2000; 2000US-0245181P.	
PA	(REGC ) UNIV CALIFORNIA.	
PA	(MART//) MARTINI A.	
XX	Martini A, Albani S, Carson DA, Prakken BJ,	
PI	WPI; 2002-489999/52.	
DR		
XX	New immunomodulatory peptides from heat shock proteins, useful for	
PT	treating immunological disorder in subjects such as humans, e.g.	
PT	autoimmune disease (e.g. arthritis), infectious disease, inflammatory	
PT	bowel disease or cancer.	
XX		
PS	Example 8; Page 53; 84pp; English.	
XX		
CC	This invention relates to the use of a peptide, which is an immunogenic	
CC	portion derived from a dnaJ heat shock protein (hsp) in modulating an	
CC	immune response in a subject. The peptides of the invention may have	
CC	immunomodulatory, cytostatic, antiinflammatory, antibacterial or	
CC	antiarthritis properties and can stimulate expression of interleukins,	
CC	tumour necrosis factor and transforming growth factor beta. The	
CC	immunogenic peptide is useful for modulating (i.e. augmenting/inducing or	
CC	reducing/inhibiting) an immune response in a subject having an	
CC	immunological disorder (e.g. autoimmune disease such as arthritis or	
CC	articular juvenile idiopathic arthritis), an infectious disease, an	
CC	inflammatory bowel disease or cancer. The immunogenic peptide of the	
CC	invention is also useful for modulating immunoeffector cell	
CC	responsiveness in a subject. The immunogenic peptide is particularly	
CC	useful for treating the above-mentioned diseases in mammals, e.g. cat,	
CC	dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In	
CC	general, the peptide is useful in methods involving mucosal toleration,	
CC	DNA vaccination, energy induction or active immunisation. The present	
CC	sequence represents the E.coli DNAJ PI immunogenic peptide of the	
CC	invention	
XX		
SQ	Sequence 15 AA;	
	Query Match 100.0%; Score 81; DB 5; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 1.3e-07;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 QKRAAYDQYGHAAFE 15	
Db	1 QKRAAYDQYGHAAFE 15	
RESULT 6		
AAE19457		
ID	AAE19457 standard; peptide; 15 AA.	
XX		
AC	AAE19457;	
XX		
DT	31-MAY-2002 (first entry)	

XX	Human heat shock protein (hsp) dnaJp1 peptide.	
DE		
XX		
KW	Human; human leukocyte antigen; HLA; DR-binding peptide; therapy;	
KW	stress protein; major histocompatibility complex; MHC; anticancer;	
KW	type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;	
KW	rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;	
KW	ulcerative colitis; infectious disease; haemostatic; nephrotropic;	
KW	polymyositis; chronic active hepatitis; primary biliary cirrhosis;	
KW	pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;	
KW	Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;	
KW	inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;	
KW	antimicrobial; immunosuppressive; dermatological; antiinflammatory;	
KW	antiinfertility; idiopathic Addison's disease; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200212286-A2.	
XX		
PD	14-FEB-2002.	
XX		
PF	08-AUG-2001; 2001WO-US041656.	
XX		
PR	09-AUG-2000; 2000US-0224104P.	
PR	06-APR-2001; 2001US-00828574.	
XX	(UYCA-) UNIV CALIFORNIA SAN DIEGO.	
PA		
XX		
PI	Albani S, Prakken BJ;	
XX		
DR	WPI; 2002-227137/28.	
XX		
PT	Novel human leukocyte antigen pan DR-binding peptide, useful for treating	
PT	immune mediated diseases and conditions, has a fragment of stress protein	
PT	that binds to major histocompatibility complex class II molecules.	
XX		
FS	Claim 9; Page 45; 68pp; English.	
XX		
CC	The invention relates to human leukocyte antigen (HLA) pan DR-binding	
CC	peptide comprising a fragment of a stress protein that binds to one or	
CC	more major histocompatibility complex (MHC) class II molecules. The	
CC	invention also relates to heat shock protein (hsp) peptides. The peptides	
CC	of the invention and thr immunomodulating composition comprising these	
CC	peptides are useful for modulating, treating or preventing an immune-	
CC	mediated disease in a mammalian subject e.g. human, having or at risk of	
CC	having a disease including autoimmune disease, multiple sclerosis (MS),	
CC	rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I	
CC	diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,	
CC	lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,	
CC	retinoblastoma, sarcoma and connective tissue cancers) and infectious	
CC	diseases. The peptides of the invention are also useful for screening	
CC	peptides or analogues that modulate pathogenic immune response. These	
CC	peptides are useful for treating autoimmune diseases or disorders	
CC	including Sjogren's syndrome, polymyositis, chronic active hepatitis,	
CC	mixed connective tissue disease, primary biliary cirrhosis, pernicious	
CC	anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,	
CC	gluten-sensitive enteropathy, Grave's disease, inflammatory bowel	
CC	disease, autoimmune neutropenia, idiopathic thrombocytopenia purpura,	
CC	pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,	
CC	bullous pemphigoid, discoid lupus and dense deposit disease. The present	
CC	sequence is human hsp dnaJp1 peptide used in the exemplification of the	
CC	invention	
XX		
SQ	Sequence 15 AA;	
	Query Match 100.0%; Score 81; DB 5; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 1.3e-07;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

## RESULT 7

ABR55132  
ID ABR55132 standard; peptide; 15 AA.  
XX  
AC ABR55132;  
XX  
DT 03-JUL-2003 (first entry)  
XX  
DE E. coli DnaJp1 antigen-specific epitope peptide.  
XX  
KW Antigen-specific epitope; immune response; T cell; cytokine;  
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;  
KW cytosolic; antithyroid; anti-asthmatic; immunosuppressive;  
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;  
KW antiallergic; dermatological; antipsoriatic.  
XX  
OS Escherichia coli.  
XX  
PN WO2003026579-A2.  
XX  
PD 03-APR-2003.  
XX  
PF 25-SEP-2002; 2002WO-US030578.  
XX  
PR 25-SEP-2001; 2001US-0325499P.  
PR 11-DEC-2001; 2001US-0339284P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Albani S, Martins A;  
XX  
DR WPI; 2003-430097/40.  
XX  
PT Modulating an immune response in a subject having an immune-related  
PT disorder, e.g. arthritis by administering an antigen-specific epitope and  
PT a cytokine or an agent that effects cytokine activity or expression.  
XX  
PS Disclosure; Page 9; 41pp; English.

XX  
XX The invention relates to a novel method for modulating an immune response  
CC in a subject having an immune-related disorder. The method comprises: (a)  
CC administering an antigen-specific epitope, where administration provides  
CC epitope-specific T cell immune modulation; and (b) administering a  
CC cytokine, an agent that effects cytokine activity or expression, or an  
CC anticytokine therapy. The method of the invention has antiarthritic,  
CC antidiabetic, neuroprotective, anti-inflammatory, cytosolic,  
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-  
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,  
CC dermatological, and antipsoriatic activity. The method is useful for  
CC modulating an immune response in a subject having an immune-related  
CC disorder. The present sequence is used in the exemplification of the  
CC invention

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
| | | | | | | | | | | | | | |  
Db 1 QKRAAYDQYGHAAFE 15

## RESULT 8

AAM99344  
ID AAM99344 standard; peptide; 16 AA.  
XX  
AC AAM99344;  
XX  
DT 07-DEC-2001 (first entry)  
XX

DE Vaccine related MHC ligand peptide SEQ ID NO:447.

XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;  
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;  
KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;  
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;  
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;  
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;  
KW human immunodeficiency virus.

XX OS Homo sapiens.

XX PN WO200170772-A2.

XX PD 27-SEP-2001.

XX PF 22-MAR-2001; 2001WO-FR000872.

XX PR 23-MAR-2000; 2000FR-00003711.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;

XX DR WPI; 2001-611470/70.

XX Stabilized pharmaceutical containing N-terminal glutamic acid or  
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
PT with strong acid.

XX PS Claim 9; Page 107; 149pp; French.

XX The present invention describes a pharmaceutical compound (I) that  
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in  
CC the form of an addition salt with a strong, physiologically acceptable  
CC acid (II). Also described are: (a) a pharmaceutical composition  
CC containing at least one (I); (b) a vaccine containing at least one (I)  
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a  
CC method for in vitro diagnosis of diseases associated with the presence of  
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process  
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,  
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and  
CC cytostatic activities. (I) are useful, in human or veterinary medicine,  
CC in pharmaceutical compositions (for treating immune disorders, e.g.  
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft  
CC rejection, infection, hormonal disorders and central nervous system  
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for  
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal  
CC infections; or (ii) of cancers. A particular application is in anti-  
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases  
CC associated with interactions between MHC and (I), e.g. melanoma and human  
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides  
CC which can be used in pharmaceutical compounds from the present invention

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
| | | | | | | | | | | | | | |  
Db 1 QKRAAYDQYGHAAFE 15

## RESULT 9

AU98852  
ID AU98852 standard; peptide; 16 AA.  
XX  
AC AU98852;  
XX  
DT 22-AUG-2002 (first entry)  
XX

```

DE XX E.Coli DNAJ 61 immunogenic peptide.
KW KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytosolic; anti-inflammatory; antibacterial; antiarthritic;
KW autoimmunity; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer;
KW mucosal toleration; DNA vaccination; anergy induction.
XX XX Escherichia coli.
OS OS WO200236611-A2.
XX XX 10-MAY-2002.
XX XX 31-OCT-2001; 2001WO-US045344.
XX XX 01-NOV-2000; 2000US-0245181P.
XX XX (REGC ) UNIV CALIFORNIA.
XX XX (MART/) MARTINI A.
XX XX Martini A, Albani S, Carson DA, Prakken BJ;
XX WPI; 2002-489999/52.
XX XX New immunomodulatory peptides from heat shock proteins, useful for
XX PT treating immunological disorder in subjects such as humans, e.g.
XX PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
XX PT bowel disease or cancer.
XX PS Claim 4; Page 55; 84pp; English.
XX XX This invention relates to the use of a peptide, which is an immunogenic
XX portion derived from a dnaJ heat shock protein (hsp) in modulating an
XX immune response in a subject. The peptides of the invention may have
XX immunomodulatory, cytosolic, anti-inflammatory, antibacterial or
XX antiarthritic properties and can stimulate expression of interleukins,
XX tumour necrosis factor and transforming growth factor beta. The
XX immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
XX reducing/inhibiting) an immune response in a subject having an
XX immunological disorder (e.g. autoimmune disease such as arthritis or
XX articular juvenile idiopathic arthritis), an infectious disease, an
XX inflammatory bowel disease or cancer. The immunogenic peptide of the
XX invention is also useful for modulating immunoreceptor cell
XX responsiveness in a subject. The immunogenic peptide is particularly
XX useful for treating the above-mentioned diseases in mammals, e.g. cat,
XX dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
XX general, the peptide is useful in methods involving mucosal toleration,
XX DNA vaccination, anergy induction or active immunisation. The present
XX sequence represents an E. coli DNAJ immunogenic peptide of the invention
XX XX
XX Sequence 16 AA;
Query Match 100.0%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAPE 15
DB 1 QKRAAYDQYGHAAPE 15
|||||
RESULT 10
ABR55126
ID ABR55126 standard; peptide; 16 AA.
XX AC ABR55126;
XX AC ABR55126;
XX DT 03-JUL-2003 (first entry)
XX DE E. coli dnaJ61 antigen-specific epitope peptide.
XX XX Antigen-specific epitope; immune response; T cell; cytokine;
KW KW

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KW KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytosolic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
XX antiallergic; dermatological; antipsoriatic.
OS OS Escherichia coli.
XX XX WO2003026579-A2.
XX XX 03-APR-2003.
XX XX 25-SEP-2002; 2002WO-US030578.
XX XX 25-SEP-2001; 2001US-0325499P.
XX XX 11-DEC-2001; 2001US-0339284P.
XX XX (REGC ) UNIV CALIFORNIA.
XX XX Albani S, Martins A;
XX WPI; 2003-430097/40.
XX XX Modulating an immune response in a subject having an immune-related
XX disorder, e.g. arthritis by administering an antigen-specific epitope and
XX a cytokine or an agent that effects cytokine activity or expression.
XX PS Disclosure; Page 9; 41pp; English.
XX XX The invention relates to a novel method for modulating an immune response
XX in a subject having an immune-related disorder. The method comprises: (a)
XX administering an antigen-specific epitope, where administration provides
XX epitope-specific T cell immune modulation; and (b) administering a
XX cytokine, an agent that effects cytokine activity or expression, or an
XX antidiabetic, neuroprotective, anti-inflammatory, cytosolic,
XX antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
XX ulcer, antianaemic, cardiant, respiratory general, antiallergic,
XX dermatological, and antipsoriatic activity. The method is useful for
XX modulating an immune response in a subject having an immune-related
XX disorder. The present sequence is used in the exemplification of the
XX invention
XX XX
XX Sequence 16 AA;
Query Match 100.0%; Score 81; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAPE 15
DB 1 QKRAAYDQYGHAAPE 15
|||||
RESULT 11
AAU02075
ID AAU02075 standard; protein; 118 AA.
XX AC AAU02075;
XX AC AAU02075;
XX DT 07-SEP-2001 (first entry)
XX DE Synthetic autoantigen shHSP/RA.
XX XX shGLP/RA; immunogenic epitope cluster; IEC;
KW synthetic human 60kDa heat shock protein; HSP60; HSP65; EcDNAJ;
KW autoantigen; autoimmune disease; multiple sclerosis;
KW rheumatoid arthritis; insulin-dependent diabetes mellitus;
KW myasthenia gravis; uveitis; autoimmune hepatitis; thyroiditis; insulinitis;
KW orchitis; idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis;
KW Mycobacterium tuberculosis heat shock protein 65; Escherichia coli DNA J.
XX XX Synthetic.
OS OS

```

OS	Homo sapiens.
OS	Escherichia coli.
OS	Mycobacterium tuberculosis.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 116
FT	/label= OTHER
FT	/note= "Other= STOP"
XX	
XX	W0200131037-A2.
PN	
PD	
XX	
XX	03-MAY-2001.
XX	
Pf	26-OCT-2000; 2000MO-IL000688.
XX	
PR	27-OCT-1999; 99IL-00132611.
XX	
PA	(YEDA ) YEDA RES & DEV CO LTD.
PI	Ben-Nun A, Kerlero De Roabo N, Sappler GP;
DR	WPI; 2001-300515/31.
DR	N-PSDB; AAS04836.
XX	
PT	Novel synthetic human target autoantigen gene useful for treating
PT	autoimmune diseases such as multiple sclerosis, insulin-dependent
PT	diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis.
XX	
XX	Claim 176; Fig 53; 182pp; English.
XX	
CC	The sequence represents SHSP/RA containing immunogenic epitope clusters
CC	(IEC) from Mycobacterium tuberculosis heat shock protein 65, Escherichia
CC	coli DNA J and human heat shock protein 60. The synthetic human target
CC	autoantigen genes of the invention comprise sequences coding for at least
CC	2 IECs of autoantigen(s) related to a specific autoimmune disease. The
CC	synthetic human target autoantigen genes are useful for treating
CC	autoimmune diseases such as multiple sclerosis, insulin-dependent
CC	diabetes mellitus, rheumatoid arthritis, myasthenia gravis, uveitis,
CC	autoimmune hepatitis, thyroiditis, insulinitis, orchitis, idiopathic
CC	thrombocytopenic purpura, and inflammatory diseases (Crohn's disease,
CC	ulcerative colitis). The synthetic human target autoantigen genes are
CC	also useful for diagnosis and/or monitoring the progression of the
CC	autoimmune disease
XX	
XX	Sequence 118 AA;
	Query Match 100.0%; Score 81; DB 4; Length 118;
	Best Local Similarity 100.0%; Pred. No. 1.2e-06;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 QKRAAYDQYGHAAFE 15
Dd	99 QKRAAYDQYGHAAFE 113
RESULT 12	
AAB11396	
ID	AAB11396 standard; protein; 131 AA.
XX	
AC	AAB11396;
XX	
DT	22-FEB-2001 (first entry)
XX	
DE	E. coli expression plasmid pUBS520-PIN-J-Domain encoded protein.
XX	
KW	Eukaryotic protein; protease; interferon; antibody; hormone;
KW	disulfide bridge.
XX	
OS	Escherichia coli.
OS	Synthetic.
XX	
PN	EP1048732-A1.
XX	
XX	
PD	02-NOV-2000.
XX	
PF	26-APR-1999; 99EP-00107412.
XX	
PR	26-APR-1999; 99EP-00107412.
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX	
WI	2000-674185/66.
DR	N-PSDB; AAC66072.
XX	
PT	Preparation of water-soluble eukaryotic polypeptides with disulfide
PT	bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT	presence of arginine or amide compound.
XX	
PS	Example 3; Page 17; 40pp; German.
XX	
CC	This invention describes a novel preparation of a water-soluble,
CC	naturally occurring eukaryotic polypeptide containing two or more
CC	cysteine units bound via a disulfide bridge which comprises cultivation
CC	of prokaryotic cells in the presence of arginine or an amide compound.
CC	The method is useful for the preparation of eukaryotic proteins e.g.
CC	proteases, interferons, protein hormones, antibodies or antibody
CC	fragments (e.g. a single chain Fv fragment that binds to thyroid
CC	stimulating hormone). It is especially useful for preparing proteins with
CC	more than five disulfide bridges, e.g. recombinant plasminogen activator
CC	(rPA). The technique is simple and does not require in vitro after-
CC	treatment, such as the removal of inclusion bodies, reduction or
CC	naturization
XX	
SQ	Sequence 131 AA;
	Query Match 100.0%; Score 81; DB 3; Length 131;
	Best Local Similarity 100.0%; Pred. No. 1.4e-06;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 QKRAAYDQYGHAAFE 15
Dd	84 QKRAAYDQYGHAAFE 98
RESULT 13	
AAB74197	
ID	AAB74197 standard; protein; 131 AA.
XX	
AC	AAB74197;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	OmpA-J domain fusion protein.
XX	
KW	Molecular chaperone; OmpA signal sequence; J domain; DnaJ.
XX	
OS	Unidentified.
XX	
FN	EP1077262-A1.
XX	
PD	21-FEB-2001.
XX	
PF	24-JUL-2000; 2000EP-00115839.
XX	
PR	29-JUL-1999; 99EP-00114811.
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX	
PI	Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX	WPI; 2001-246712/26.
DR	N-PSDB; AAF77804.
XX	
XX	
PT	Producing naturally folded eukaryotic proteins e.g. antibodies,
PT	interferon, hormones or proteases that contain two or several cysteines
PT	linked by disulfide bridges comprises co-expression of a molecular

PT chaperone.  
XX  
PS Disclosure; Page 14; 35pp; English.  
XX  
CC The present invention relates to a method for production of a naturally  
CC folded eukaryotic protein containing two or more cysteines linked by  
CC disulfide bridges. The method comprises co-expression and secretion into  
CC the periplasm of a molecular chaperone via an expression vector coding  
CC for the chaperone. The expression vector also encodes a signal sequence.  
CC The method is useful for producing a naturally folded eukaryotic protein  
CC such as an antibody, antibody fragment, interferon, protein hormone or a  
CC protease containing two or several cysteines linked by disulfide bridges.  
CC The present sequence is a fusion protein composed of the OmpA signal  
CC sequence and the J domain of DnaJ. This sequence was used in the method  
CC of the present invention  
XX  
SQ Sequence 131 AA;  
  
Query Match 100.0%; Score 81; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QKRAAYDOYGHAAFE 15  
DB 84 QKRAAYDOYGHAAFE 98  
|||||  
QY 1 QKRAAYDOYGHAAFE 15  
DB 84 QKRAAYDOYGHAAFE 98  
|||||  
  
RESULT 15  
AAY72018  
ID AAY72018 standard; protein; 131 AA.  
XX  
AC AAY72018;  
XX  
DT 28-MAR-2001 (first entry)  
XX  
DE E. coli OmpA-J domain fusion protein encoded by PUBS520-pIN-J-domain.  
XX  
KW Secreted protein; chaperone; interferon; protease; hormone;  
KW fusion protein; naturally folded protein; lac-lpp promoter; DnaJ;  
KW heat shock protein; HSP; outer membrane protein A; OmpA; J domain.  
XX  
OS Escherichia coli.  
XX  
PN EP1054063-A2.  
XX  
PD 22-NOV-2000.  
XX  
PF 19-APR-2000; 2000EP-00108505.  
XX  
PR 26-APR-1999; 99EP-00107412.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX  
PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
XX  
DR WPI; 2001-033777/05.  
DR N-PSDB; AAD02210.  
XX  
PT Producing water-soluble, naturally folded, and secreted eukaryotic  
PT polypeptide, involves culturing prokaryotic cells containing an  
PT expression vector encoding the polypeptide in the presence of arginine or  
PT a specific compound.  
XX  
PS Example 3; Page 17; 35pp; English.  
XX  
CC The patent discloses a method for the production of a water-soluble,  
CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.  
CC The method involves culturing the prokaryotic cells, containing an  
CC expression vector encoding the desired protein and the prokaryotic signal  
CC sequence, in the presence of an additive, e.g., L-arginine. The signal  
CC sequence mediates the secretion of the desired protein into the  
CC periplasm, where folding of the protein takes place. The prokaryotic cell  
CC also contains an expression vector encoding a molecular chaperone, e.g.,  
CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-  
CC overexpression and co-secretion of molecular chaperones in the periplasm  
CC improves the yield of functionally folded protein. The above method  
CC recombinantly produces a high yield of eukaryotic secreted proteins in  
CC prokaryotes. The method is useful for producing eukaryotic proteins such  
CC as an antibody, antibody fragment, interferon, protein hormone or a  
CC protease. The present sequence is an Escherichia coli outer membrane  
CC protein A (OmpA) signal sequence-J domain fusion protein encoded by  
CC PUBS520-pIN-J-domain. The plasmid, PUBS520-pIN-J-domain, also contains  
CC the lac-lpp promoter and the lpp terminator. The periplasmic co-secretion  
CC of J domain, which is the N-terminal portion of the DnaJ, facilitates the  
CC folding of the desired secreted protein  
XX

PT chaperone.  
XX  
PS Disclosure; Page 14; 35pp; English.  
XX  
CC The present invention relates to a method for production of a naturally  
CC folded eukaryotic protein containing two or more cysteines linked by  
CC disulfide bridges. The method comprises co-expression and secretion into  
CC the periplasm of a molecular chaperone via an expression vector coding  
CC for the chaperone. The expression vector also encodes a signal sequence.  
CC The method is useful for producing a naturally folded eukaryotic protein  
CC such as an antibody, antibody fragment, interferon, protein hormone or a  
CC protease containing two or several cysteines linked by disulfide bridges.  
CC The present sequence is a fusion protein composed of the OmpA signal  
CC sequence and the J domain of DnaJ. This sequence was used in the method  
CC of the present invention  
XX  
SQ Sequence 131 AA;  
  
Query Match 100.0%; Score 81; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QKRAAYDOYGHAAFE 15  
DB 84 QKRAAYDOYGHAAFE 98  
|||||  
QY 1 QKRAAYDOYGHAAFE 15  
DB 84 QKRAAYDOYGHAAFE 98  
|||||  
  
RESULT 14  
AAB70767  
ID AAB70767 standard; protein; 131 AA.  
XX  
AC AAB70767;  
XX  
DT 18-MAY-2001 (first entry)  
XX  
DE Expression plasmid PUBS520-pIN-J-domain protein.  
XX  
KW Chaperone protein; periplasm; antibody production; protein production;  
KW interferon production; protease production.  
XX  
OS Escherichia coli.  
OS Synthetic.  
XX  
PN EP1077263-A1.  
XX  
PD 21-FEB-2001.  
XX  
PF 29-JUL-1999; 99EP-00114811.  
XX  
PR 29-JUL-1999; 99EP-00114811.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX  
DR WPI; 2001-204356/21.  
DR N-PSDB; AAF61191.  
XX  
PT Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by  
PT simultaneous expression of a chaperone protein, allows simple recovery  
PT from periplasm or medium.  
XX  
PS Disclosure; Page 15; 36pp; German.  
XX  
CC This invention describes a novel method for preparing a naturally folded  
CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged  
CC Cys residues by culturing prokaryotic cells that contain an expression  
CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
CC periplasm. (I) is secreted into the periplasm or medium; the signal  
CC peptide is then cleaved and (I) isolated from the periplasm or medium.  
CC The method is used for production of antibody, interferon, protein  
CC hormone or protease. Expression of (III) increases the yield of (I). The  
CC method is simple and eliminates time-consuming in vitro processing and  
CC operations such as dissolution of inclusion bodies, reduction and





PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI: 2001-465460/50.  
DR N-PSDB; AAS27505.  
XX  
PT Novel polypeptides useful for diagnosing, treating, preventing and/or  
PT prognosing disorders related to the proteins, including cancers, immune  
PT disorders and neuronal disorders.  
XX  
PS Claim 1; SEQ ID NO 1153; 800pp; English.  
XX  
CC The invention relates to novel isolated polypeptides (I), and  
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
CC diagnosing, preventing and treating diseases including immune system  
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
CC transplant rejections and graft versus host disease, infectious diseases  
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
CC other blood-related disorders (sickle cell anaemia), myeloproliferative  
CC disorders, primary haematopoietic disorders, hyperproliferative disorders  
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities  
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
CC respiratory disorders, dermatological disorders, in wound healing,  
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's  
CC disease), reproductive system disorders, gastrointestinal disorder  
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
CC B-cell responsiveness to pathogens, activators of T-cells, to induce  
CC higher affinity antibodies, and as a means to induce tumour proliferation  
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-  
CC AAU17683 represent novel signal transduction pathway protein, amino acid  
CC sequences of the invention  
XX

Query Match 100.0%; Score 81; DB 4; Length 340;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15

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25 QKRAAYDQYGHAAFE 39  
RESULT 17  
ADB94296  
ID ADB94296 standard; protein; 340 AA.  
XX AC ADB94296;  
XX 04-DEC-2003 (first entry)  
XX Human novel protein #530.  
XX human; autoimmune disease; Parkinson's disease; silicosis;  
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;  
KW immunosuppressive agent; adjuvant; enhance immune response;  
KW higher affinity antibody induction;  
KW increased serum immunoglobulin concentration.  
XX OS Homo sapiens.  
XX US2002168711-A1.  
XX 14-NOV-2002.  
XX 17-JAN-2001; 2001US-00764868.  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 07-JUL-2000; 2000US-0216647P.  
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PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
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PR 02-OCT-2000; 2000US-0237038P.  
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PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.  
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 XX (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 XX  
 XX Rosen CA, Ruben SM, Barash SC;  
 XX  
 XX WPI; 2003-719985/68.  
 DR N-PSDB; ADB93673.  
 XX  
 PT New isolated polypeptide useful for diagnosing and treating  
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's  
 PT disease.  
 XX  
 PS Claim 11; SEQ ID NO 1153; 345pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide. The polypeptide is  
 CC useful for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, by determining the presence or  
 CC amount of expression of the polypeptide in a biological sample and  
 CC diagnosing a pathological condition or a susceptibility to a pathological  
 CC condition based on the presence or amount of expression of the  
 CC polypeptide. The polypeptide is also useful for identifying a binding  
 CC partner to the polypeptide, which involves contacting the polypeptide  
 CC with a binding partner and determining whether the binding partner  
 CC effects an activity of the polypeptide. The polypeptide or the nucleic  
 CC acid encoding the polypeptide is useful for preventing, treating, or  
 CC ameliorating a medical condition, which involves administering the  
 CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid  
 CC is useful for diagnosing a pathological condition or a susceptibility to  
 CC a pathological condition in a subject, which involves determining the  
 CC presence or absence of a mutation in the nucleic acid, and diagnosing a  
 CC pathological condition or susceptibility to a pathological condition  
 CC based on the presence or absence of the mutation. The polypeptide, the  
 CC nucleic acid and an antibody to the polypeptide are useful for treating  
 CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal  
 CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,  
 CC the nucleic acid and the antibody are useful as immunosuppressive agents,  
 CC as adjuvants to enhance immune responses, and as agents to induce higher  
 CC affinity antibodies and increase serum immunoglobulin concentrations. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC protein. Note: The sequence data for this patent did not form part of the  
 CC printed specification but was obtained in electronic format direct from  
 CC USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.  
 XX  
 SQ Sequence 340 AA;  
 Query Match 100.0%; Score 81; DB 7; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 Db 25 QKRAAYDQYGHAAFE 39  
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 RESULT 18  
 AAU17587  
 ID AAU17587 standard; protein; 341 AA.  
 XX  
 AC AAU17587;  
 XX  
 XX 07-NOV-2001 (first entry)  
 XX  
 DE Novel signal transduction pathway protein, Seq ID 1152.  
 XX  
 XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;  
 KW

KW immune system disorder; rheumatoid arthritis; inflammatory condition;  
 KW organ transplant rejection; infection; hepatitis C; blood disorder;  
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
 KW reproductive system; gastrointestinal; liver disorder; AIDS;  
 KW acquired immune deficiency syndrome.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200154733-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US001312.  
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 XX 31-JAN-2000; 2000US-0179065P.  
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PR 17-NOV-2000; 2000US-0249246P.
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PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465460/50.
XX N-ESDB; AAS27504.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cancers, immune
XX disorders and neuronal disorders.
XX
XX Claim 1; SEQ ID NO 1152; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative disorders
XX (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
XX Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (e.g.
XX Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
XX glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
XX respiratory disorders, dermatological disorders (e.g. Addison's
XX epithelial cell proliferation, endocrine disorders, gastrointestinal disorder
XX (disease), reproductive system disorders, liver disorders, cirrhosis), as stimulators of
XX (inflammatory disorders), as activators of T-cells, to induce
XX B-cell responsiveness to pathogens, and as a means to induce tumour proliferation
XX higher affinity antibodies, and as a means to induce tumour proliferation
XX in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
XX AAU17683 represent novel signal transduction pathway protein, amino acid
XX sequences of the invention
XX

Query Match 100.0%; Score 81; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 26 QKRAAYDQYGHAAFE 40

RESULT 19
ADB94295
ID ADB94295 standard; protein; 341 AA.
XX
XX ADB94295;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human novel protein #529.
XX
XX human; autoimmune disease; Parkinson's disease; silicosis;
XX gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
XX immunosuppressive agent; adjuvant; enhance immune response;
XX higher affinity antibody induction;
XX increased serum immunoglobulin concentration.
XX
XX Homo sapiens.
XX
XX US2002168711-A1.
PR
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XX PD 14-NOV-2002.  
XX PF 17-JAN-2001; 2001US-00764868.  
XX PR 31-JAN-2000; 2000US-0179065P.  
XX PR 04-FEB-2000; 2000US-0180628P.  
XX PR 28-JUN-2000; 2000US-0214886P.  
XX PR 07-JUL-2000; 2000US-0216647P.  
XX PR 07-JUL-2000; 2000US-0216880P.  
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XX PR 14-JUL-2000; 2000US-0217486P.  
XX PR 14-JUL-2000; 2000US-0218230P.  
XX PR 26-JUL-2000; 2000US-0220963P.  
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XX PR 14-AUG-2000; 2000US-0224518P.  
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XX PR 14-AUG-2000; 2000US-0225447P.  
XX PR 14-AUG-2000; 2000US-0225757P.  
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XX PR 02-OCT-2000; 2000US-0237039P.  
XX PR 13-OCT-2000; 2000US-0237040P.  
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XX PR 17-NOV-2000; 2000US-0249299P.  
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XX PR 08-DEC-2000; 2000US-0251869P.  
XX (ROSE/) ROSEN C A.  
XX (RUBE/) RUBEN S M.  
XX (BARA/) BARASH S C.  
XX PI Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2003-719985/68.  
XX N-PSDB; ADB93672.  
XX New isolated polypeptide useful for diagnosing and treating  
PT immunosuppressive conditions such as autoimmune disease and Parkinson's  
PT disease.  
XX Claim 11; SEQ ID NO 1152; 345pp; English.  
XX The invention relates to an isolated polypeptide. The polypeptide is  
CC useful for diagnosing a pathological condition or a susceptibility to a

CC pathological condition in a subject, by determining the presence or  
CC amount of expression of the polypeptide in a biological sample and  
CC diagnosing a pathological condition or a susceptibility to a pathological  
CC condition based on the presence or amount of expression of the  
CC polypeptide. The polypeptide is also useful for identifying a binding  
CC partner to the polypeptide, which involves contacting the polypeptide  
CC with a binding partner and determining whether the binding partner  
CC effects an activity of the polypeptide. The polypeptide or the nucleic  
CC acid encoding the polypeptide is useful for preventing, treating, or  
CC ameliorating a medical condition, which involves administering the  
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid  
CC is useful for diagnosing a pathological condition or a susceptibility to  
CC a pathological condition in a subject, which involves determining the  
CC presence or absence of a mutation in the nucleic acid, and diagnosing a  
CC pathological condition or susceptibility to a pathological condition  
CC based on the presence or absence of the mutation. The polypeptide, the  
CC nucleic acid and an antibody to the polypeptide are useful for treating  
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal  
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,  
CC the nucleic acid and the antibody are useful as immunosuppressive agents,  
CC as adjuvants to enhance immune responses, and as agents to induce higher  
CC affinity antibodies and increase serum immunoglobulin concentrations. The  
CC present sequence represents the amino acid sequence of a novel human  
CC protein. Note: The sequence data for this patent did not form part of the  
CC printed specification but was obtained in electronic format direct from  
CC USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.  
XX  
XX SQ Sequence 341 AA;  
Query Match 100.0%; Score 81; DB 7; Length 341;  
Best Local Similarity 100.0%; Pred. No. 4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYGHAAFE 15  
DB 26 OKRAAYDQYGHAAFE 40  
RESULT 20  
ABM67485  
ID ABM67485 standard; protein; 373 AA.  
XX AC ABM67485;  
XX DT 20-NOV-2003 (first entry)  
XX DE Photorhabdus luminescens protein sequence #582.  
XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
XX whooping cough.  
XX OS Photorhabdus luminescens.  
XX PN WO200294867-A2.  
XX PD 28-NOV-2002.  
XX PF 07-FEB-2002; 2002WO-IB003040.  
XX PR 07-FEB-2001; 2001PR-00001659.  
XX (INSP ) INST PASTEUR.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX WPI; 2003-148459/14.  
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX PS Claim 2; SEQ ID NO 582; 1205pp; French.

XX CC The invention relates to the isolation of genes and their encoded

XX CC proteins from Photorhabdus luminescens. The isolated sequences are

XX CC sources of probes and primers for detecting the genome of P. luminescens

XX CC and related species; to study polymorphisms; for gene analysis and for

XX CC detection/amplification of the genes. Antibodies (Ab) raised against the

XX CC polypeptides encoded by the genes are used for detection/identification

XX CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

XX CC carry a gene-containing vector are used to select compounds that

XX CC modulate, regulate, induce or inhibit expression of the genes in plants,

XX CC animals or microorganisms other than P. luminescens and are able to alter

XX CC response or sensitivity to toxins and antibiotics produced by P.

XX CC luminescens. Cells transformed to express the genes are useful for

XX CC recombinant production of the proteins, particularly toxins and

XX CC antibacterials useful as insecticides, bactericides and fungicides. The

XX CC genes, proteins, vectors containing the genes and Ab are also useful

XX CC therapeutically (to treat microbial infection by bacteria or fungi that

XX CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as

XX CC biopesticides. Other uses of the genes and the proteins are as virulence

XX CC factors and for identifying targets of human diseases for which P.

XX CC luminescens is a model (particularly plague and whooping cough). This

XX CC sequence represents one of the isolated P. luminescens proteins

XX SQ Sequence 373 AA;

Query Match 100.0%; Score 81; DB 6; Length 373;

Best Local Similarity 100.0%; Pred. No. 4.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 QKRAAYDQYGHAAFE 75

RESULT 21

ADNR89339

ID ADNR89339 standard; protein; 376 AA.

AC ADNR89339;

XX 18-NOV-2004 (first entry)

DT E. coli protein-folding-related factor, DnaJ.

DE PFRF; protein-folding-related factor; chaperone; GroES; GroEL; DnaK;

XX DnaJ; GrpE; gene function; cell-free synthesis;

XX recombinant protein production; therapeutic protein.

XX Escherichia coli.

XX WO2004072107-A1.

XX 26-AUG-2004.

XX 13-FEB-2004; 2004WO-KR000302.

XX 15-FEB-2003; 2003KR-00009628.

XX (DREA-) DREAMBIOGEN CO LTD.

XX Kang SH, Choi WJ, Kim HJ, Jun SY, Lee KY;

XX WPI; 2004-616042/59.

XX Producing soluble proteins using transformed genes encoding protein-

XX folding-related factors in a cell-free protein synthesis system, useful

XX in therapeutic, industrial and research purposes.

XX Example 1; SEQ ID NO 4; 58pp; English.

XX The invention relates to producing soluble protein. The method involves

CC preparing cells transformed by genes encoding protein-folding-related

CC factors (PFRF), so that the transformed cells can express enhanced levels

CC of the PFRFs, over-expressing the factors and preparing a cell extract

CC for a cell-free protein synthesis system from the transformed cells, and

CC producing a high level of soluble protein in the synthesis system

CC containing the extract containing the factors. The folding-related factor

CC in producing a soluble protein is one or more in number, and/or is a

CC chaperone that is GroES/GroEL chaperone family or DnaK/DnaJ/GrpE

CC chaperone family. The cell extract is prepared from one or more

CC transformed cells. The protein is alpha, beta, gamma-interferon, lipase,

CC erythropoietin, cytokines, interleukins, granulocyte-colony stimulating

CC factor, granulocyte macrophage-colony stimulating factor, transforming

CC growth factors, thrombopoietin, or tissue plasminogen activator. The

CC methods and compositions of the present invention are useful for

CC producing soluble proteins applicable to therapeutic, industrial and

CC research purposes, in particular for assaying functions of newly

CC discovered genes. The present sequence represents the amino acid sequence

CC of an E. coli DnaJ, a protein-folding-related factor.

XX SQ Sequence 376 AA;

Query Match 100.0%; Score 81; DB 8; Length 376;

Best Local Similarity 100.0%; Pred. No. 4.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDQYGHAAFE 75

RESULT 22

ADNR18036

ID ADNR18036 standard; protein; 376 AA.

XX ADNR18036;

XX 02-DEC-2004 (first entry)

DT Bacterial polypeptide #689.

DE Recombinant DNA construct; transformed plant; improved plant property;

XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

XX pathogen tolerance; pest tolerance; plant disease resistance;

XX cell cycle pathway modification; plant growth regulator;

XX homologous recombination; seed oil yield; protein yield; carbohydrate;

XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

XX for expression of a polynucleotide encoding a polypeptide from a

XX microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 689; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 376 AA;

Query Match 100.0%; Score 81; DB 8; Length 376;  
 Best Local Similarity 100.0%; Pred. NO. 4.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 |||||  
 DB 61 QKRAAYDQYGHAAFE 75

RESULT 23  
 ADN17733  
 ID ADN17733 standard; protein; 378 AA.

XX AC ADN17733;  
 XX 02-DEC-2004 (first entry)  
 XX Bacterial polypeptide #386.  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.  
 XX US2003233675-A1.  
 XX 18-DEC-2003.  
 XX 20-FEB-2003; 2003US-00369493.  
 XX 21-FEB-2002; 2002US-0360039P.  
 XX (CAOY/) CAO Y.  
 XX (HINK/) HINKLE G J.  
 XX (SLAT/) SLATER S C.  
 XX (CHEN/) CHEN X.  
 XX (GOLD/) GOLDMAN B S.

71 Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 386; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 378 AA;

Query Match 100.0%; Score 81; DB 8; Length 378;  
 Best Local Similarity 100.0%; Pred. NO. 4.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 |||||  
 DB 61 QKRAAYDQYGHAAFE 75

RESULT 24  
 ADS42875  
 ID ADS42875 standard; protein; 378 AA.

XX AC ADS42875;  
 XX 02-DEC-2004 (first entry)  
 XX Bacterial polypeptide #21305.  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.  
 XX US2003233675-A1.  
 XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.  
 XX 21-FEB-2002; 2002US-0360039P.  
 XX (CAOY/) CAO Y.

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PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 21305; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 378 AA;
XX
XX Query Match 100.0%; Score 81; DB 8; Length 378;
XX Best Local Similarity 100.0%; Pred. NO. 4.4e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGHAAFE 15
XX | | | | | | | | | | | | | | |
XX Db 61 QKRAAYDQYGHAAFE 75
XX
XX RESULT 25
XX ADF05627
XX ID ADF05627 standard; protein; 380 AA.
XX
XX AC ADF05627;
XX
XX AD 29-JUL-2004 (first entry)
XX
XX DE Klebsiella pneumoniae polypeptide seqid 9011.
XX
XX KW Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX OS Klebsiella pneumoniae.
XX
XX PN US6610836-B1.
XX
XX PD 26-AUG-2003.
XX
XX PF 27-JAN-2000; 2000US-00489039.
XX
XX PR 29-JAN-1999; 99US-0117747P.
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Breton GL, Osborne M;
XX
XX DR WPI; 2003-895346/82.
XX
XX N-PSDB; ACH96045.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX Disclosure; SEQ ID NO 9011; 932pp; English.
XX
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XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL;
XX
XX WPI; 2003-895291/82.
XX N-PSDB; ADF01455.
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
XX reagents for diagnosis of bacterial disease, as components of
XX antibacterial vaccines, as targets for antibacterial drugs, or as
XX biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 5912; 870pp; English.
XX
XX The invention relates to new Proteus mirabilis polypeptides and
XX polynucleotides. The invention also relates to antibodies against the
XX polypeptides. Methods for producing the polypeptides, a method of
XX generating vaccines for immunising an individual against P. mirabilis, a
XX method for evaluating a compound for the ability to bind a P. mirabilis
XX polypeptide and a method for screening test compounds for anti-bacterial
XX activity. The polypeptides and polynucleotides are useful as molecular
XX targets for diagnosing, preventing and treating pathological conditions
XX resulting from bacterial infection, as reagents for diagnosis of
XX bacterial diseases, as components of antibacterial vaccines, as targets
XX for antibacterial drugs or as bio-control agents for plants. This
XX sequence represents a Proteus mirabilis polypeptide of the invention.
XX
XX Sequence 380 AA;
XX
XX Query Match 100.0%; Score 81; DB 7; Length 380;
XX Best Local Similarity 100.0%; Pred. NO. 4.5e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGHAAFE 15
XX | | | | | | | | | | | | | | |
XX Db 63 QKRAAYDQYGHAAFE 77
XX
XX RESULT 26
XX ABO62494
XX ID ABO62494 standard; protein; 380 AA.
XX
XX AC ABO62494;
XX
XX AD 29-JUL-2004 (first entry)
XX
XX DE Klebsiella pneumoniae polypeptide seqid 9011.
XX
XX KW Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX OS Klebsiella pneumoniae.
XX
XX PN US6610836-B1.
XX
XX PD 26-AUG-2003.
XX
XX PF 27-JAN-2000; 2000US-00489039.
XX
XX PR 29-JAN-1999; 99US-0117747P.
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Breton GL, Osborne M;
XX
XX DR WPI; 2003-895346/82.
XX
XX N-PSDB; ACH96045.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX Disclosure; SEQ ID NO 9011; 932pp; English.
XX
```



XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition  
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
 CC Klebsiella pneumoniae polypeptide of the invention  
 XX  
 SQ Sequence 380 AA;

Query Match 100.0%; Score 81; DB 7; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
 DB 64 OKRAAYDQYGHAAFE 78

RESULT 27  
 AAB11395  
 ID AAB11395 standard; protein; 399 AA.  
 XX  
 AC AAB11395;  
 XX  
 XX 22-FEB-2001 (first entry)  
 XX  
 XX

DE E. coli expression plasmid pUBS20-pIN-dnaJ encoded protein.  
 XX

KW Eukaryotic protein; protease; interferon; antibody; hormone;  
 KM disulfide bridge.  
 XX

OS Escherichia coli.  
 OS Synthetic.  
 XX

PN EP1048732-A1.  
 XX

XX 02-NOV-2000.  
 PD

XX 26-APR-1999; 99EP-00107412.  
 PF

XX 26-APR-1999; 99EP-00107412.  
 PR

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA

XX WPI; 2000-674185/66.  
 DR

XX N-PSDB; AAC66071.  
 DR

XX Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.  
 PT

XX Example 2; Page 13-15; 40pp; German.  
 PS

XX This invention describes a novel preparation of a water-soluble,  
 CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain Fv fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 CC naturalization  
 CC

XX Sequence 399 AA;  
 SQ

Query Match 100.0%; Score 81; DB 3; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
 DB 84 OKRAAYDQYGHAAFE 98

RESULT 28  
 AAB74196  
 ID AAB74196 standard; protein; 399 AA.  
 XX  
 AC AAB74196;  
 XX  
 XX 29-MAY-2001 (first entry)  
 XX  
 XX OmpA-DnaJ fusion protein.  
 DE  
 XX Molecular chaperone; OmpA signal sequence; DnaJ.  
 XX

XX Unidentified.  
 OS

XX EP1077262-A1.  
 PN

XX 21-FEB-2001.  
 PD

XX 24-JUL-2000; 2000EP-00115839.  
 PF

XX 29-JUL-1999; 99EP-00114811.  
 PR

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA

XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 PI

XX WPI; 2001-246712/26.  
 DR

XX N-PSDB; AAF77803.  
 DR

XX Producing naturally folded eukaryotic proteins e.g. antibodies,  
 PT interferon, hormones or proteases that contain two or several cysteines  
 PT linked by disulfide bridges comprises co-expression of a molecular  
 PT chaperone.  
 PT

XX Disclosure; Page 11-12; 35pp; English.  
 PS

XX The present invention relates to a method for production of a naturally  
 CC folded eukaryotic protein containing two or more cysteines linked by  
 CC disulfide bridges. The method comprises co-expression and secretion into  
 CC the periplasm of a molecular chaperone via an expression vector coding  
 CC for the chaperone. The expression vector also encodes a signal sequence.  
 CC The method is useful for producing a naturally folded eukaryotic protein  
 CC such as an antibody, antibody fragment, interferon, protein hormone or a  
 CC protease containing two or several cysteines linked by disulfide bridges.  
 CC The present sequence is a fusion protein composed of the OmpA signal  
 CC sequence and DnaJ. This sequence was used in the method of the present  
 CC invention  
 CC

XX Sequence 399 AA;  
 SQ

Query Match 100.0%; Score 81; DB 4; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
 DB 84 OKRAAYDQYGHAAFE 98

RESULT 29  
 AAB70766  
 ID AAB70766 standard; protein; 399 AA.  
 XX  
 AC AAB70766;  
 XX

XX 18-MAY-2001 (first entry)  
 DT  
 XX

DE Expression plasmid pUBS520-pIN-dnaJ protein.  
 XX Chaperone protein; periplasm; antibody production; protein production;  
 KW interferon production; protease production.  
 XX Escherichia coli.  
 OS Synthetic.  
 XX EP1077263-A1.  
 XX 21-FEB-2001.  
 XX 29-JUL-1999; 99EP-00114811.  
 XX 29-JUL-1999; 99EP-00114811.  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX WPI; 2001-204356/21.  
 DR N-PSDB; AAF61190.  
 XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by  
 PT simultaneous expression of a chaperone protein, allows simple recovery  
 PT from periplasm or medium.  
 XX Disclosure; Page 11-13; 36pp; German.  
 XX This invention describes a novel method for preparing a naturally folded  
 CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged  
 CC Cys residues by culturing prokaryotic cells that contain an expression  
 CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
 CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
 CC periplasm. (I) is secreted into the periplasm or medium; the signal  
 CC peptide is then cleaved and (I) isolated from the periplasm or medium.  
 CC The method is used for production of antibody, interferon, protein  
 CC hormone or protease. Expression of (III) increases the yield of (I). The  
 CC method is simple and eliminates time-consuming in vitro processing  
 CC operations such as dissolution of inclusion bodies, reduction and  
 CC refolding. (III) protects (I) against agglomeration and promotes their  
 CC natural conformation  
 XX Sequence 399 AA;  
 SQ  
 Query Match 100.0%; Score 81; DB 4; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 OKRAAYDQYGHAAFE 15  
 DB 84 QKRAAYDQYGHAAFE 98  
 RESULT 30  
 AA72017  
 ID AA72017 standard; protein; 399 AA.  
 AC AA72017;  
 XX 28-MAR-2001 (first entry)  
 DT E. coli OmpA-DnaJ fusion protein encoded by pUBS520-pIN-dnaJ.  
 DE  
 XX Secreted protein; chaperone; interferon; protease; hormone;  
 KW fusion protein; naturally folded protein; lac-ipp promoter; DnaJ;  
 KW heat shock protein; HSP; outer membrane protein A; OmpA.  
 XX Escherichia coli.  
 OS  
 XX EP1054063-A2.  
 XX 22-NOV-2000.  
 XX 19-APR-2000; 2000EP-00108505.  
 PF

XX 26-APR-1999; 99EP-00107412.  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 XX WPI; 2001-033777/05.  
 DR N-PSDB; AAD02209.  
 XX Producing water-soluble, naturally folded, and secreted eukaryotic  
 PT polypeptide, involves culturing prokaryotic cells containing an  
 PT expression vector encoding the polypeptide in the presence of arginine or  
 PT a specific compound.  
 XX Example 2; Page 13-15; 35pp; English.  
 XX The patent discloses a method for the production of a water-soluble,  
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.  
 CC The method involves culturing the prokaryotic cells, containing an  
 CC expression vector encoding the desired protein and the prokaryotic signal  
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal  
 CC sequence mediates the secretion of the desired protein into the  
 CC periplasm, where folding of the protein takes place. The prokaryotic cell  
 CC also contains an expression vector encoding a molecular chaperone, e.g.,  
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-  
 CC overexpression and co-secretion of molecular chaperones in the periplasm  
 CC improves the yield of functionally folded protein. The above method  
 CC recombinantly produces a high yield of eukaryotic secreted proteins in  
 CC prokaryotes. The method is useful for producing eukaryotic proteins such  
 CC as an antibody, antibody fragment, interferon, protein hormone or a  
 CC protease. The present sequence is an Escherichia coli outer membrane  
 CC protein A (OmpA) signal sequence-dnaJ fusion protein encoded by pUBS520-  
 CC pIN-dnaJ. The plasmid, pUBS520-pIN-dnaJ, also contains the lac-ipp  
 CC promoter and the ipp terminator. The periplasmic co-secretion of DnaJ  
 CC facilitates the folding of the desired secreted protein  
 XX Sequence 399 AA;  
 SQ  
 Query Match 100.0%; Score 81; DB 4; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 OKRAAYDQYGHAAFE 15  
 DB 84 QKRAAYDQYGHAAFE 98  
 RESULT 31  
 AAU02077  
 ID AAU02077 standard; protein; 459 AA.  
 XX AAU02077;  
 AC  
 XX 07-SEP-2001 (first entry)  
 DT Synthetic multi-target autoantigen Y-RAPb.  
 DE  
 XX Y-RAPa; immunogenic epitope cluster; IEC; autoantigen; shCollagen/RA;  
 KW shagrecan/RA; shGLP/RA; shHSP/RA; autoimmune disease;  
 KW multiple sclerosis; rheumatoid arthritis;  
 KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;  
 KW autoimmune hepatitis; thyroiditis; insulinitis; orchitis;  
 KW idiopathic thrombocytopenic purpura; inflammatory disease;  
 KW Crohn's disease; ulcerative colitis; shMultiTAG.  
 XX Synthetic.  
 OS Homo sapiens.  
 OS Escherichia coli.  
 OS Mycobacterium tuberculosis.  
 XX Key Location/Qualifiers  
 FH Misc-difference 455  
 FT

FT /label= OTHER  
 FT /note= "Other= STOP"  
 FT Misc-difference 457  
 FT /label= OTHER  
 FT /note= "Other= STOP"

XX WO200131037-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-IL000698.

XX 27-OCT-1999; 99IL-00132611.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Ben-Nun A, Kerlero De Rosbo N, Sappier GP;

XX WPI; 2001-300515/31.

XX N-PSDB; AAS04838.

XX Novel synthetic human target autoantigen gene useful for treating  
 PT autoimmune diseases such as multiple sclerosis, insulin-dependent  
 PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis.

XX Claim 182; Fig 57; 182pp; English.

XX The sequence represents synthetic human multi-target autoantigen  
 CC (shMultitrag) Y-RAPA consisting of regions encoding shCollagen/RA,  
 CC shAggrecan/RA, shGLP/RA and shHSP/RA. The synthetic human target  
 CC autoantigen genes of the invention comprise sequences coding for at least  
 CC 2 IECs of autoantigen(s) related to a specific autoimmune disease. The  
 CC synthetic human target autoantigen genes are useful for treating  
 CC autoimmune diseases such as multiple sclerosis, insulin-dependent  
 CC diabetes mellitus, rheumatoid arthritis, myasthenia gravis, uveitis,  
 CC autoimmune hepatitis, thyroiditis, insulinitis, orchitis, idiopathic  
 CC thrombocytopenic purpura, and inflammatory diseases (Crohn's disease,  
 CC ulcerative colitis). The synthetic human target autoantigen genes are  
 CC also useful for diagnosis and/or monitoring the progression of the  
 CC autoimmune disease

XX SQ Sequence 459 AA;

Query Match 100.0%; Score 81; DB 4; Length 459;

Best Local Similarity 100.0%; Pred. No. 5.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 440 QKRAAYDQYGHAAFE 454

RESULT 32

ABG17771

ID ABG17771 standard; protein; 476 AA.

AC ABG17771;

XX 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #17762.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

OS WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS81958.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 20; SEQ ID NO 48130; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABC0010-ABG30377 represent novel human diagnostic

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 476 AA;

Query Match 100.0%; Score 81; DB 4; Length 476;

Best Local Similarity 100.0%; Pred. No. 5.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 81 QKRAAYDQYGHAAFE 95

RESULT 33

ADS21615

ID ADS21615 standard; protein; 365 AA.

XX ADS21615;

XX 02-DEC-2004 (first entry)

DE Bacterial polypeptide #10648.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX Bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.



XX WPI; 2004-061375/06.  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 12087; 122pp; English.  
 XX  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 376 AA;

Query Match 90.1%; Score 73; DB 8; Length 376;  
 Best Local Similarity 86.7%; Pred. No. 0.00012;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
 |||||:|||||  
 Db 60 QKRAAYDRFGHAAPE 74

RESULT 36  
 AAR95446  
 ID AAR95446 standard; peptide; 15 AA.

XX AAR95446;  
 XX  
 DT 01-JUL-1996 (first entry)

XX RA susceptibility sequence peptide #2.

XX Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;  
 KW arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus;  
 KW Klebsiella; Proteus; therapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 1..5  
 FT /note= "rheumatoid arthritis susceptibility sequence"

FT Misc-difference 1 /note= "Q1D"

FT Misc-difference 2 /note= "K2E"

XX WO9531984-A1.  
 XX 30-NOV-1995.

XX

PF 24-APR-1995; 95WO-US004896.  
 XX  
 PR 20-MAY-1994; 94US-00246988.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Carson DA, Salvatore A;  
 XX  
 XX WPI; 1996-020344/02.

XX Treatment of rheumatoid arthritis - by limiting exposure of immune system  
 PT to arthritogenic peptide(s).

XX Example 3; Page 36; 52pp; English.

XX AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility  
 CC sequence (see AAR95443 and AAR95444) containing peptides. This sequence  
 CC corresponds to a region of dnaJ. These sequences are present on  
 CC arthritogenic proteins and are targeted in this invention as antibody  
 CC recognition sites. The anti-arthritogenic peptide antibodies that are  
 CC developed can then be administered to a patient who has RA or who is  
 CC predisposed to develop RA, to reduce the exposure to arthritogenic  
 CC peptides. The antibodies are produced and administered in milk. An  
 CC alternative treatment method comprises the administration of a non-  
 CC adsorbable antibiotic, together with a RA-beggn bacteria (selected from  
 CC the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the  
 CC patient who has RA (or a predisposition to it). Candidates for either of  
 CC these methods can be screened by detecting an in-vitro cellular immune  
 CC response to an arthritogenic peptide. The method of the invention allows  
 CC for the reduction of sensitisation to microbial arthritogenic peptides  
 CC (such as dnaJ). It also limits the exposure of the systemic immune system  
 CC of humans to RA arthritogenic peptides present in the gastrointestinal  
 CC tract  
 XX  
 SQ Sequence 15 AA;

Query Match 88.9%; Score 72; DB 2; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 5.5e-06;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAPE 15  
 :|||||  
 Db 2 ERAAYDQYGHAAPE 15

RESULT 37  
 AAW25796  
 ID AAW25796 standard; peptide; 15 AA.

XX AAW25796;

XX  
 DT 06-APR-1998 (first entry)

XX Peptide dnaJpV which protects against arthritogenic peptides.

XX dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;  
 KW arthritogenic peptide; autoimmune disease; systemic immune system;  
 KW anti-dnaJp1 antibody; passive immunisation;  
 KW rheumatoid arthritis-susceptibility detection.

XX Synthetic.

XX Escherichia coli.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= Q1D

FT /note= "wild type Gln substituted with Asp"

FT Misc-difference 2 /label= K2E

FT /note= "wild type Lys substituted with Glu"

XX WO9734002-A1.

XX

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PD 18-SEP-1997.
XX
XX
PF 20-FEB-1997; 97WO-US002957.
XX
XX
PR 15-MAR-1996; 96US-00618464.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Carson DA, Albani S;
XX
XX WPI; 1997-470882/43.
XX
XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
PT - also determining pre-disposition to rheumatoid arthritis by detecting
PT anti-arthritogenic peptide antibodies.
XX
XX Disclosure; Page 5; 44pp; English.
XX
XX Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
CC relatively strong immune response in seropositive adult rheumatoid
CC arthritis patients. This peptide was used in a vaccine for protecting
CC against arthritogenic peptides. The vaccine contains a carrier, pure
CC dnaJp1 peptide or a recombinant gene expression vector encoding the
CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
CC other autoimmune diseases). Vaccines can target the arthritogenic
CC peptides before they are presented to the systemic immune system. Anti-
CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies
CC can be used to detect rheumatoid arthritis-susceptibility sequences on
CC HLA or in populations of E. coli in the gastrointestinal tract
XX
XX Sequence 15 AA;
SQ
Query Match 88.9%; Score 72; DB 2; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.5e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db :|||||
2 ERAAYDQYGHAAFE 15

RESULT 38
AAE19458
ID AAE19458 standard; peptide; 15 AA.
AC
XX AAE19458;
XX
XX 31-MAY-2002 (first entry)
XX
XX Heat shock protein (hsp) dnaJpV peptide.
XX
XX Human leukocyte antigen; HLA; DR-binding peptide; therapy;
KW stress protein; major histocompatibility complex; MHC; antiulcer;
KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
KW ulcerative colitis; infectious disease; haemostatic; nephrotropic;
KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
KW inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
KW antiinfertility; idiopathic Addison's disease; cytostatic.
XX
XX Unidentified.
XX
XX WO200212286-A2.
XX
XX 14-FEB-2002.
XX
XX 08-AUG-2001; 2001WO-US041656.
XX
XX 09-AUG-2000; 2000US-0224104P.
XX
XX
PR 06-APR-2001; 2001US-00828574.
XX
XX (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX
XX Albani S, Prakken BJ;
XX
XX WPI; 2002-227137/28.
XX
XX Novel human leukocyte antigen pan DR-binding peptide, useful for treating
PT immune mediated diseases and conditions, has a fragment of stress protein
PT that binds to major histocompatibility complex class II molecules.
XX
XX Example 3; Page 46; 68pp; English.
XX
XX The invention relates to human leukocyte antigen (HLA) pan DR-binding
CC peptide comprising a fragment of a stress protein that binds to one or
CC more major histocompatibility complex (MHC) class II molecules. The
CC invention also relates to heat shock protein (hsp) peptides. The peptides
CC of the invention and the immunomodulating composition comprising these
CC peptides are useful for modulating, treating or preventing an immune-
CC mediated disease in a mammalian subject e.g. human, having or at risk of
CC having a disease including autoimmune disease, multiple sclerosis (MS),
CC rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
CC diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
CC lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
CC reinoblastoma, sarcoma and connective tissue cancers) and infectious
CC diseases. The peptides of the invention are also useful for screening
CC peptides or analogues that modulate pathogenic immune response. These
CC peptides are useful for treating autoimmune diseases or disorders
CC including Sjogren's syndrome, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
CC anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
CC gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
CC disease, autoimmune neutropaenia, idiopathic thrombocytopenia purpura,
CC pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
CC bullous pemphigoid, discoid lupus and dense deposit disease. The present
CC sequence is hsp dnaJpV peptide used in the exemplification of the
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 88.9%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.5e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db :|||||
2 ERAAYDQYGHAAFE 15

RESULT 39
ABR55133
ID ABR55133 standard; peptide; 15 AA.
XX
XX ABR55133;
XX
XX 03-JUL-2003 (first entry)
XX
XX E. coli dnaJpV antigen-specific epitope peptide.
XX
XX Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cycostatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianemic; cardiac; respiratory;
KW antiallergic; dermatological; antipsoriatic.
XX
XX Escherichia coli.
XX
XX WO2003026579-A2.
XX
XX 03-APR-2003.
XX
XX 25-SEP-2002; 2002WO-US030578.
XX
XX

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XX 25-SEP-2001; 2001US-0325499P.  
 PR 11-DEC-2001; 2001US-0339284P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Albani S, Martins A;  
 XX WPI; 2003-430097/40.  
 DR Modulating an immune response in a subject having an immune-related  
 PT disorder, e.g. arthritis by administering an antigen-specific epitope and  
 PT a cytokine or an agent that effects cytokine activity or expression.  
 XX Disclosure; Page 9; 41pp; English.  
 XX The invention relates to a novel method for modulating an immune response  
 CC in a subject having an immune-related disorder. The method comprises: (a)  
 CC administering an antigen-specific epitope, where administration provides  
 CC epitope-specific T cell immune modulation; and (b) administering a  
 CC cytokine, an agent that effects cytokine activity or expression, or an  
 CC anticytokine therapy. The method of the invention has antiarthritic,  
 CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,  
 CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-  
 CC ulcer, antianaemic, cardiac, respiratory general, antiallergic,  
 CC dermatological, and antiposoriatic activity. The method is useful for  
 CC modulating an immune response in a subject having an immune-related  
 CC disorder. The present sequence is used in the exemplification of the  
 CC invention  
 XX SQ Sequence 15 AA;  
 Query Match 88.9%; Score 72; DB 6; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 5.5e-06;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 KRAAYDQYGHAAFE 15  
 Db :|||||:|||||  
 2 ERAAYDQYGHAAFE 15  
 RESULT 40  
 ID ADN25412 standard; protein; 382 AA.  
 AC ADN25412;  
 XX 02-DEC-2004 (first entry)  
 DE Bacterial polypeptide #8065.  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX Bacteria.  
 OS (CAOY/) CAO Y.  
 XX (HINK/) HINKLE G J.  
 PA (SLATY/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 XX 20-FEB-2003; 2003US-00369493.  
 XX 21-FEB-2002; 2002US-0360039P.  
 XX (CAOY/) CAO Y.  
 XX (HINK/) HINKLE G J.  
 PA (SLATY/) SLATER S C.  
 PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.  
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 DR New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX Claim 1; SEQ ID NO 8065; 122pp; English.  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX SQ Sequence 382 AA;  
 Query Match 85.2%; Score 69; DB 8; Length 382;  
 Best Local Similarity 85.7%; Pred. No. 0.00067;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 KRAAYDQYGHAAFE 15  
 Db :|||||:|||||  
 62 KRAAYDQYGHAAFE 75  
 RESULT 41  
 ID ADS43419 standard; protein; 384 AA.  
 XX ADS43419;  
 AC ADS43419;  
 XX 02-DEC-2004 (first entry)  
 DE Bacterial polypeptide #21849.  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX Bacteria.  
 OS US2003233675-A1.  
 XX 18-DEC-2003.  
 PD 20-FEB-2003; 2003US-00369493.  
 PF

PF	28-FEB-2003; 2003US-00375010.
PP	
XX	28-FEB-2003; 2003US-00375010.
XX	
XX	(AJIN ) AJINOMOTO CO INC.
XX	
PI	Usuda Y, Nishio Y, Yasueda H, Sugimoto S;
XX	
DR	WPI; 2004-642012/62.
DR	N-PSDB; ADR31367.
XX	
PT	New isolated polynucleotides encoding polypeptides involved in central
PT	intermediates metabolism in Methylophilus methylotrophus, useful for
PT	producing amino acids with improved yield in microorganisms.
XX	
XX	Claim 41; SEQ ID NO 22; 49pp; English.
XX	
CC	The invention describes an isolated polynucleotide (I) encoding a protein
CC	comprising 180, 552, 250, 104, 95, 649, 246, 258, 516, 639, 376, 629,
CC	170, 545, 95, 539 or 105 amino acids (PI)-(PI7), fully defined in the
CC	specification, and comprising a sequence of 543, 1659, 753, 315, 288,
CC	1350, 741, 777, 1551, 1920, 1131, 1890, 513, 1638, 288, 1620, or 318 base
CC	pairs (SI)-(S17), fully defined in the specification. Also described are:
CC	a vector comprising at least one isolated (I); a host cell comprising at
CC	least one isolated (I); detecting a polynucleotide with at least 70%
CC	homology to (I); producing a polynucleotide with at least 70% homology to
CC	(I); production of a protein which comprises culturing the host cell for
CC	a time and under conditions suitable for expression of the protein and
CC	collecting the produced protein; production of at least one amino acid
CC	which comprises culturing the host cell for a time and under conditions
CC	suitable for producing the amino acid and collecting the produced amino
CC	acid; an isolated polynucleotide (II), which hybridises under stringent
CC	conditions to at least one isolated polynucleotide (S1)-(S17); a vector
CC	comprising (II); a host cell comprising (II); an isolated polynucleotide
CC	(III) which is at least 95% identical to the polynucleotide (S1)-(S17); a
CC	vector comprising (III); a host cell comprising (III); an isolated
CC	polypeptide (IV) comprising (PI)-(PI7), and an isolated polypeptide at
CC	least 95% identical to (IV). The polynucleotides are useful as probes to
CC	isolate and/or identify RNA, cDNA, and DNA molecules, particularly for
CC	producing amino acids with improved yield in microorganisms. This is the
CC	amino acid sequence of DnaJ, a protein involved in stress response to
CC	environmental changes.
XX	
XX	Sequence 376 AA;
XX	
XX	Query Match 82.7%; Score 67; DB 8; Length 376;
XX	Best Local Similarity 80.0%; Pred. No. 0.0015;
XX	Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX	
Qy	1 QKRAAYDQYGHAAPE 15
XX	
Db	63 QKRAAYDQYGHAGVD 77
XX	
RESULT 43	
ADN24677	
ID	ADN24677 standard; protein; 379 AA.
XX	
AC	ADN24677;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Bacterial polypeptide #7330.
XX	
KW	Recombinant DNA construct; transformed plant; improved plant property;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW	pathogen tolerance; pest tolerance; plant disease resistance;
KW	cell cycle pathway modification; plant growth regulator;
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW	bacterial polypeptide.
OS	Bacteria.



XX PN US2003233675-A1.  
 XX KW 18-DEC-2003.  
 PD XX  
 XX PF 20-FEB-2003; 2003US-00369493.  
 XX PR 21-FEB-2002; 2002US-0360039P.  
 XX PA (CAOY/) CAO Y.  
 XX PA (HINK/) HINKLE G J.  
 XX PA (SLAT/) SLATER S C.  
 XX PA (CHEN/) CHEN X.  
 XX PA (GOLD/) GOLDMAN B S.  
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 7330; 122pp; English.  
 XX  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition. Improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 XX Sequence 379 AA;  
 SQ  
 Query Match 82.7%; Score 67; DB 8; Length 379;  
 Best Local Similarity 80.0%; Pred. No. 0.0015;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 Db ||||| :  
 61 QKRAAYDQYGHAGVD 75  
 RESULT 44  
 ADN21920  
 ID ADN21920 standard; protein; 380 AA.  
 XX  
 AC ADN21920;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 XX Bacterial polypeptide #4573.  
 DE  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW

KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 XX US2003233675-A1.  
 XX PN  
 XX 18-DEC-2003.  
 PD XX  
 XX PF 20-FEB-2003; 2003US-00369493.  
 XX PR 21-FEB-2002; 2002US-0360039P.  
 XX PA (CAOY/) CAO Y.  
 XX PA (HINK/) HINKLE G J.  
 XX PA (SLAT/) SLATER S C.  
 XX PA (CHEN/) CHEN X.  
 XX PA (GOLD/) GOLDMAN B S.  
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 4573; 122pp; English.  
 XX  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition. Improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 XX Sequence 380 AA;  
 SQ  
 Query Match 82.7%; Score 67; DB 8; Length 380;  
 Best Local Similarity 80.0%; Pred. No. 0.0015;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 Db ||||| :  
 61 QKRAAYDQYGHAGVD 75  
 RESULT 45  
 AAR95445  
 ID AAR95445 standard; peptide; 14 AA.  
 XX  
 AC AAR95445;

XX 01-JUL-1996 (first entry)  
 XX RA susceptibility sequence peptide #1.  
 XX Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;  
 KW arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus;  
 KW Klebsiella; Proteus; therapy.  
 XX Escherichia coli.  
 XX  
 XX Key Location/Qualifiers  
 FH Region 1..5  
 FT /note= "rheumatoid arthritis susceptibility sequence"  
 XX  
 XX WO9531984-A1.  
 XX 30-NOV-1995.  
 XX 24-APR-1995; 95WO-US004896.  
 XX 20-MAY-1994; 94US-00246988.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Carson DA, Salvatore A;  
 XX WPI; 1996-020344/02.  
 XX Treatment of rheumatoid arthritis - by limiting exposure of immune system  
 PT to arthritogenic peptide(s).  
 XX Example 3; Page 36; 52pp; English.  
 XX AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility  
 CC sequence (see AAR95443 and AAR95444) containing peptides. This sequence  
 CC corresponds to a region of dnaJ. These sequences are present on  
 CC arthritogenic proteins and are targeted in this invention as antibody  
 CC recognition sites. The anti-arthritogenic peptide antibodies that are  
 CC developed can then be administered to a patient who has RA or who is  
 CC predisposed to develop RA, to reduce the exposure to arthritogenic  
 CC peptides. The antibodies are produced and administered in milk. An  
 CC alternative treatment method comprises the administration of a non-  
 CC adsorbable antibiotic, together with a RA-beggn bacteria (selected from  
 CC the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the  
 CC patient who has RA (or a predisposition to it). Candidates for either of  
 CC these methods can be screened by detecting an in-vitro cellular immune  
 CC response to an arthritogenic peptide. The method of the invention allows  
 CC for the reduction of sensitisation to microbial arthritogenic peptides  
 CC (such as dnaJ). It also limits the exposure of the systemic immune system  
 CC of humans to RA arthritogenic peptides present in the gastrointestinal  
 CC tract  
 XX Sequence 14 AA;  
 SQ  
 Query Match 79.6%; Score 64.5; DB 2; Length 14;  
 Best Local Similarity 93.3%; Pred. No. 0.00012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 OKRAAYDQYGHAAFE 15  
 Db 1 OKRAAYDQY-HAAFE 14  
 RESULT 46  
 ADN17394  
 ID ADN17394 standard; protein; 376 AA.  
 XX  
 XX ADN17394;  
 XX  
 XX 02-DEC-2004 (first entry)  
 XX Bacterial polypeptide #47.  
 DE

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 XX bacterial polypeptide.  
 XX Bacteria.  
 XX OS  
 XX US2003233675-A1.  
 XX 18-DEC-2003.  
 XX 20-FEB-2003; 2003US-00369493.  
 XX 21-FEB-2002; 2002US-0360039P.  
 XX (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 PI WPI; 2004-061375/06.  
 DR  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX Claim 1; SEQ ID NO 47; 122pp; English.  
 PS  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX Sequence 376 AA;  
 SQ  
 Query Match 77.8%; Score 63; DB 8; Length 376;  
 Best Local Similarity 73.3%; Pred. No. 0.008;  
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 OKRAAYDQYGHAAFE 15  
 Db 63 EKKLYDMYGHAAFE 77  
 RESULT 47  
 ADO25512



PR 08-NOV-2002; 2002US-0425201P.  
PR 12-MAR-2003; 2003US-0453914P.  
PR 12-MAR-2003; 2003US-0454021P.  
PR 12-MAR-2003; 2003US-0454128P.  
PR 12-MAR-2003; 2003US-0454193P.  
PR 13-MAR-2003; 2003US-0454215P.  
PR 13-MAR-2003; 2003US-0454218P.  
PR 13-MAR-2003; 2003US-0454487P.  
PR 13-MAR-2003; 2003US-0454507P.  
PR 13-MAR-2003; 2003US-0454536P.  
PR 14-MAR-2003; 2003US-0455010P.  
PR 14-MAR-2003; 2003US-0455036P.  
PR 14-MAR-2003; 2003US-0455054P.  
PR 14-MAR-2003; 2003US-0455082P.  
PR 17-MAR-2003; 2003US-0455191P.  
PR 17-MAR-2003; 2003US-0455192P.  
PR 17-MAR-2003; 2003US-0455334P.  
PR 17-MAR-2003; 2003US-0455335P.  
PR 17-MAR-2003; 2003US-0455343P.  
XX (AFFI-) AFFINIUM PHARM INC.  
XX  
XX Edwards A, Dharamsi A, Vedadi M, Domagala M, Nethery K;  
PI Mansoury K, Pinder B, Alam MZ, Ng I, Virag C, Houston S;  
PI McDonald M, Buzadzija K;  
XX  
DR WPI; 2004-400642/37.  
DR N-PSDB; ADO25509.  
XX  
XX Bacterial polypeptide composition useful for treating bacterial  
PT infection, has isolated, recombinant bacterial polypeptide such as GTP-  
PT binding protein Era from *Pseudomonas aeruginosa* or *adenylosuccinate lyase*  
PT from *Enterococcus faecalis*.  
XX  
XX Claim 44; SEQ ID NO 185; 566pp; English.  
PS  
XX This invention relates to the identification of novel protein targets for  
CC the development of antimicrobial drugs against pathogenic bacteria.  
CC Specifically, it refers to recombinant proteins derived from  
CC *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*,  
CC *Escherichia coli*, *Enterococcus faecalis* or *Pseudomonas aeruginosa*. The  
CC present invention describes providing a three-dimensional structure for  
CC these crystallised proteins to identify a potential modulator for the  
CC prevention or treatment of microbial diseases. Furthermore, contacting a  
CC protein with a modulator can be useful for assaying protein activity and  
CC hence its viability in drug composition or vaccine. Accordingly, such  
CC compositions can be useful for treating bacterial infections, developing  
CC antibacterial agents useful as food preservatives or treating food  
CC products to eliminate potential pathogens. This polypeptide sequence is a  
CC bacterial protein target of the invention.  
XX  
SQ Sequence 389 AA;  
Query Match 77.8%; Score 63; DB 8; Length 389;  
Best Local Similarity 91.7%; Pred. No. 0.0083;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KRKAAYDQYQYCHA 12  
Db 61 QKKAAYDQYQYCHA 72  
||:|||||  
||:|||||  
RESULT 49  
ADS24625  
ID ADS24625 standard; protein; 374 AA.  
XX  
XX ADS24625;  
AC  
XX  
XX 02-DEC-2004 (first entry)  
DT  
XX Bacterial polypeptide #13658.  
DE  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX US2003233675-A1.  
PN 18-DEC-2003.  
PD  
XX 20-FEB-2003; 2003US-00369493.  
PF  
XX 21-FEB-2002; 2002US-0360039P.  
PR  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
DR  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 13658; 122pp; English.  
PS  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 374 AA;  
Query Match 76.5%; Score 62; DB 8; Length 374;  
Best Local Similarity 78.6%; Pred. No. 0.012;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 KRAAYDQYGHAAFE 15  
Db 62 KRAAYDQYGHAGVD 75  
|||||  
|||||  
RESULT 50  
ABO78428  
ID ABO78428 standard; protein; 381 AA.  
XX

AC AB078428;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa polypeptide #10603.  
 XX  
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US6551795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US-0074788P.  
 PR 27-JUL-1998; 98US-0094190P.  
 XX  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA  
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 PI  
 XX WPI; 2003-615309/58.  
 DR  
 DR N-ESDB; ABD11999.  
 XX  
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 27174; 455pp; English.  
 XX  
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences AB067826-  
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 381 AA;  
 Query Match 76.5%; Score 62; DB 7; Length 381;  
 Best Local Similarity 78.6%; Pred. No. 0.012;  
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 KRAAYDQYGHAAFE 15  
 |||||  
 Db 66 KRAAYDQYGHAGVD 79  
 RESULT 51  
 ADN25797  
 ID ADN25797 standard; protein; 378 AA.  
 XX  
 AC ADN25797;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #8450.  
 XX  
 KW Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 PN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 XX (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 PI  
 XX WPI; 2004-061375/06.  
 DR  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 PS Claim 1; SEQ ID NO 8450; 122pp; English.  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 378 AA;  
 Query Match 75.3%; Score 61; DB 8; Length 378;  
 Best Local Similarity 66.7%; Pred. No. 0.018;  
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 OKRAAYDQYGHAAFE 15  
 |||||  
 Db 61 EKRAAYDQYGHAGVD 75  
 RESULT 52  
 ADN10662  
 ID ADN10662 standard; protein; 385 AA.  
 XX  
 AC ADN10662;  
 XX

DT 20-NOV-2003 (first entry)  
 XX  
 DE Alloicoccus otitis antigenic protein SEQ ID NO:4398.  
 XX  
 KW Alloicoccus otitis; antigenic protein; immunogenic; immunisation;  
 KW gene therapy; Gram-positive bacterium; infection.  
 XX  
 OS Alloicoccus otitis.  
 XX  
 PN WO2003048304-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-US036123.  
 XX  
 PR 29-NOV-2001; 2001US-0333777P.  
 PR 18-NOV-2002; 2002US-0426742P.  
 XX  
 PA (AMHP) WYETH HOLDINGS CORP.  
 XX  
 PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;  
 XX  
 WPI: 2003-505284/47.  
 DR N-PSDB; ADB10665.  
 DR  
 XX New Alloicoccus otitis polynucleotides and polypeptides, useful for  
 PT treating and diagnosing diseases, drug screening assays and monitoring of  
 PT effects during drug clinical trials.  
 XX  
 PS Claim 33; SEQ ID NO 4398; 1019pp; English.  
 XX  
 CC The present invention describes an isolated polynucleotide (I) of  
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.  
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)  
 CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
 CC expression vector comprising the novel isolated polynucleotide (I), its  
 CC complement, degenerate variant or fragment; (3) a genetically engineered  
 CC host cell, transfected, transformed or infected with the vector of (2);  
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
 CC composition comprising the polypeptide, its complement, biological  
 CC equivalent or fragment, or the polynucleotide that is comprised in the  
 CC expression vector; (6) a pharmaceutical composition comprising the  
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
 CC immunising against Alloicoccus otitis by administering to a host the  
 CC immunogenic composition; (9) detecting and/or identifying Alloicoccus  
 CC otitis in the biological sample; (10) a kit comprising a container  
 CC containing the novel polynucleotide, its degenerate variant or fragment,  
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
 CC genetically engineered host cell under conditions suitable to produce the  
 CC polypeptide from the culture. (I) can be used in gene therapy. The  
 CC polynucleotides, polypeptides, antibodies and compositions of the present  
 CC invention can be used for treating and diagnosing diseases, drug  
 CC screening assays and monitoring of effects during drug clinical trials.  
 CC The polynucleotides are useful for expressing and detecting Alloicoccus  
 CC otitis. The present sequence represents an Alloicoccus otitis  
 CC antigen protein from the present invention.  
 XX  
 SQ Sequence 385 AA;  
 Query Match 75.3%; Score 61; DB 6; Length 385;  
 Best Local Similarity 91.7%; Pred. No. 0.019;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KRAAYDQYGHAA 13  
 DB |||||:||||  
 62 KRAAYDRYGHAA 73  
 RESULT 53  
 ADS26826  
 ID ADS26826 standard; protein; 375 AA.  
 XX

AC ADS26826;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #15859.  
 XX  
 KW Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 PN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX  
 WPI: 2004-061375/06.  
 XX  
 CC New recombinant DNA construct comprising a promoter positioned to provide  
 CC for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source, useful for producing plants with improved properties.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 15859; 122pp; English.  
 CC  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 375 AA;  
 Query Match 74.1%; Score 60; DB 8; Length 375;  
 Best Local Similarity 78.6%; Pred. No. 0.028;  
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 KRAAYDQYGHAAE 15  
 |||||:|||||

Db 62 KRRAYDAHGHAAPF 75

RESULT 54  
ADS26454

ID ADS26454 standard; protein; 376 AA.

XX AC

XX ADS26454;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #15487.

XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 15487; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC having an improved property comprising transforming a plant with the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition. Improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 376 AA;

Query Match 74.1%; Score 60; DB 8; Length 376;  
Best Local Similarity 78.6%; Pred. No. 0.028; 2; Indels 0; Gaps 0;  
Matches 11; Conservative 1; Mismatches 2;

QY 2 KRAAYDOYGHAAPE 15  
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Db 62 KRRAYDAHGHAAPF 75

## RESULT 55

ADN26988

ID ADN26988 standard; protein; 358 AA.

XX AC

XX ADN26988;

XX DT

XX 02-DEC-2004 (first entry)

XX DE

XX Bacterial polypeptide #9641.

XX KW

KW Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

XX OS

XX Bacteria.

XX PN

XX US2003233675-A1.

XX PD

XX 18-DEC-2003.

XX PF

XX 20-FEB-2003; 2003US-00369493.

XX PR

XX 21-FEB-2002; 2002US-0360039P.

XX PA

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX PI

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR

XX WPI; 2004-061375/06.

XX PT

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX XX

XX Claim 1; SEQ ID NO 9641; 122pp; English.

XX CC

XX The invention relates to a recombinant DNA construct comprising a

XX promoter functional in a plant cell, where the promoter is positioned to

XX provide for expression of a polynucleotide encoding a polypeptide from a

XX microbial source. The invention also relates to a transformed plant

XX comprising the recombinant DNA construct and a method of producing a

XX transformed plant having an improved property. The plant is a crop plant

XX such as maize or soybean. The method of producing a transformed plant

XX having an improved property comprises transforming a plant with the

XX recombinant DNA construct and growing the transformed plant, where the

XX polynucleotide or polypeptide is useful for improving plant properties.

XX The recombinant DNA construct is useful for producing plants with

XX improved plant properties, e.g. improved cold, heat or drought tolerance,

XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

XX increased resistance to plant disease, better growth rate by modification

XX of the cell cycle pathway with plant growth regulators, increased rate of

XX homologous recombination, modified seed oil or protein yield and/or

XX content, improved yield by modification of carbohydrate, nitrogen or

XX phosphorus use and/or uptake, by modification of photosynthesis or by

XX providing improved plant growth and development under at least one stress

XX CC

CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 358 AA;

Query Match 72.8%; Score 59; DB 8; Length 358;  
Best Local Similarity 66.7%; Pred. No. 0.04;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQVGHAAPE 15  
:|||||:|:|:  
Db 46 EKKARYDQMGHSAFD 60

RESULT 56

AAG14804  
ID AAG14804 standard; protein; 332 AA.

XX

AC AAG14804;

XX

DT 17-OCT-2000 (first entry)

XX

Arabidopsis thaliana protein fragment SEQ ID NO: 14804.

XX

Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX

Arabidopsis thaliana.

XX

EP1033405-A2.

XX

06-SEP-2000.

XX

25-FEB-2000; 2000EP-00301439.

XX

25-FEB-1999; 99US-0121825P.

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05-MAR-1999; 99US-0123180P.

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09-MAR-1999; 99US-0123548P.

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23-MAR-1999; 99US-0125788P.

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29-MAR-1999; 99US-0126785P.

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06-APR-1999; 99US-0128234P.

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08-APR-1999; 99US-0128714P.

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16-APR-1999; 99US-0129845P.

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21-APR-1999; 99US-0130449P.

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23-APR-1999; 99US-0130510P.

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30-APR-1999; 99US-0132048P.

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04-MAY-1999; 99US-0132484P.

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05-MAY-1999; 99US-0132485P.

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06-MAY-1999; 99US-0132486P.

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11-MAY-1999; 99US-01324863P.

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PR 04-OCT-1999; 99US-0157117P.  
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PR 28-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 332;  
Best Local Similarity 66.7%; Pred. No. 0.056;  
Matches 10; Conservative 2; Mismatches 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
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Db 26 EKRDLYDQFGHEAFE 40  
  
RESULT 57  
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AC AAG14803;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14803.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PR 26-OCT-1999; 99US-0161360P.  
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PR 28-OCT-1999; 99US-0161920P.  
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PR 29-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 367;  
Best Local Similarity 66.7%; Pred. No. 0.062;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QKRAAYDQGHAAFE 15  
: ||| : ||| |||

Db 61 EKRDLYDQFGHEAPE 75

RESULT 58  
ABBS5579

ID ABB5579 standard; protein; 379 AA.

XX AC ABB5579;

XX 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX Lactococcus lactis protein dhaj.

DE XX

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

KW XX

OS Lactococcus lactis; IL1403.

XX PN FR2807446-A1.

XX PD 12-OCT-2001.

XX 11-APR-2000; 2000FR-00004630.

XX 11-APR-2000; 2000FR-00004630.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.

PA Bolotine A, Sorokine A, Renault P, Ehrlich SD;

PI WPI; 2002-043418/06.

DR XX

XX New nucleotide sequence useful in the identification or Lactococcus

PT lactis and related species.

XX Claim 6; SEQ ID NO 2281; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide

CC sequence (ABA90521) and related proteins (ABBS53300-ABBS5621). The nucleic

CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related

CC species. The proteins of the invention are useful for the biosynthesis or

CC biodegradation of a composition of interest. The invention helps research

CC in lactic bacteria, particularly useful in the production of yogurt and

CC cheese. Note: The sequence data for this patent is based on equivalent

CC patent WO2001/77334 (published 18-OCT-2001) which is available in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to

CC standardise OS field)

XX SQ Sequence 379 AA;

Query Match 71.6%; Score 58; DB 5; Length 379;

Best Local Similarity 91.7%; Pred. No. 0.065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGEA 12

Db 60 QKRAAYDQYGEA 71

RESULT 59

ADS29490

ID ADS29490 standard; protein; 379 AA.

XX AC ADS29490;

XX 02-DEC-2004 (first entry)

DT XX

XX Bacterial polypeptide #18523.

DE XX

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

pathogen tolerance; pest tolerance; plant disease resistance;

cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

XX PN 18-DEC-2003.

PD 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

DR XX

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 18523; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the

CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 379 AA;

Query Match 71.6%; Score 58; DB 8; Length 379;

Best Local Similarity 91.7%; Pred. No. 0.065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGEA 12

Db 60 QKRAAYDQYGEA 71

RESULT 60

ADS27721

ID ADS27721 standard; protein; 385 AA.

XX ADS27721;

XX 02-DEC-2004 (first entry)  
XX Bacterial polypeptide #16754.  
XX  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
XX Bacteria.  
XX  
XX US2003233675-A1.  
XX  
XX 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
XX  
XX 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 16754; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: the sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
XX Sequence 385 AA;  
SQ  
Query Match 71.6%; Score 58; DB 8; Length 385;  
Best Local Similarity 83.3%; Pred. No. 0.066;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 OKRAAYDOYGH 12  
DB 59 QKRAAYDRFGHA 70

RESULT 61  
AAG14802  
ID AAG14802 standard; protein; 456 AA.  
XX  
XX AAG14802;  
AC AAG14802;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14802.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS  
XX EPI033405-A2.  
FN  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127452P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0132863P.  
PR 14-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 30-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142115P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142300P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144894P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145119P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 28-JUL-1999; 99US-0145952P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147316P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149388P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.

PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 71.6%; Score 58; DB 3; Length 456;  
Best Local Similarity 66.7%; Pred. No. 0.079;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 150 EKRDLYDQFGHAAFE 164  
RESULT 62  
ADS30613  
ID ADS30613 standard; protein; 369 AA.  
XX  
AC ADS30613;

02-DEC-2004 (first entry)  
Bacterial polypeptide #19646.  
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; call cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.  
Bacteria.  
US2003233675-A1.  
18-DEC-2003.  
20-FEB-2003; 2003US-00369493.  
21-FEB-2002; 2002US-0360039P.  
(CAOY/) CAO Y.  
(HINK/) HINKLE G J.  
(SLAT/) SLATER S C.  
(CHEN/) CHEN X.  
(GOLD/) GOLDMAN B S.  
CAO Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
WPT; 2004-061375/06.  
New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.  
Claim 1; SEQ ID NO 19646; 122pp; English.  
The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
Sequence 369 AA;  
SQ

RESULT_63	
ABB48799	ABB48799 standard; protein; 377 AA.
XX	
AC	ABB48799;
XX	
DT	05-FEB-2002 (first entry)
XX	
DE	Listeria monocytogenes protein #1503.
XX	
DE	Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW	vitamin B12; bacterial infection; disease.
KW	
OS	Listeria monocytogenes.
XX	
PN	WO200177335-A2.
XX	
PD	18-OCT-2001.
XX	
PF	11-APR-2001; 2001WO-FR001118.
XX	
PR	11-APR-2000; 2000FR-00004629.
XX	
PA	(INSP ) INST PASTEUR.
XX	Buchrieser C, Frangeul L, Couve E, Rueniock C, Faihi H, Dehoux P;
PI	Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst P, Coscart P;
PI	Daniels J, Gobel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI	Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI	Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI	Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI	Madueno E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;
PI	Rose M, Voss H;
XX	
DR	WPI; 2002-010914/01.
XX	
PT	Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT	and prevention of Listeria and related bacterial infections, and related
PT	polypeptides.
XX	
PS	Claim 6; SEQ ID NO 1504; 192pp; French.
XX	
CC	The present invention relates to the genome sequence of Listeria
CC	monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC	it are useful for selecting probes and primers for detecting genes in L.
CC	monocytogenes and related organisms, and for studying genetic
CC	polymorphisms and other genomes. The present sequence is a protein
CC	encoded by the genome sequence of the present invention. Proteins
CC	expressed from the genome sequence are useful for raising specific
CC	antibodies, identification of L. monocytogenes and related organisms, and
CC	for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC	B12. The genome sequence and proteins encoded by it are also useful for
CC	selecting compounds that regulate gene expression and cell replication
CC	and modulate L. monocytogenes-related diseases. In addition, the genome
CC	sequence and proteins encoded by it are useful in pharmaceutical and
CC	vaccines compositions for the treatment or prevention of infections by L.
CC	monocytogenes and related organisms. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 377 AA;
XX	

```

RESULT 64
AAW22358
ID AAW22358 standard; protein; 352 AA.
XX
AC AAW22358;
XX
DT 01-OCT-1997 (first entry)
XX
DE S. pneumoniae N-terminal portion of DnaJ protein.
XX
KW Streptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP72;
KW open reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric;
KW E. coli; Lactococcus lactis; antibody; vaccine; infection; human.
XX
OS Streptococcus pneumoniae.
XX
FN W09640928-A1.
XX
PD 19-DEC-1996.
XX
PF 17-MAY-1996; 96WO-CA000322.
XX
PR 07-JUN-1995; 95US-00472534.
PR 04-AUG-1995; 95US-0001805P.
XX
PA (IAFB-) IAF BIOVAC INC.
XX
PI Hamel J, Brodeur B, Martin D, Rioux C;
XX
WPI; 1997-052328/05.
DR N-PSDB; AAT73388.
XX
PT Streptococcal heat shock proteins and corresponding DNA sequences - used
PT in the production of a vaccine to treating and preventing strain-specific
PT Streptococcal infection.
XX
PS Example 3; Page 93-94; 156pp; English.
XX
CC This amino acid sequence corresponds to the N-terminal portion of the
CC Streptococcus pneumoniae DnaJ protein. The protein shows a high degree of
CC identity (72% and 51%) to the DnaJ proteins from Lactococcus lactis and
CC E. coli respectively. The sequence encoding this truncated protein was
CC isolated on the same nucleotide sequence that encodes the S. pneumoniae
CC heat shock protein 72 (HSP72; AAW22357). The nucleotide fragment was
CC isolated from a HindIII-partially digested genomic DNA library using a
CC fragment of the chimaeric gene (AA773392) corresponding to the sequence
CC encoding the C-terminal 169 amino acids of HSP72. The HSP72 protein and
CC its fragment, or antibodies specific to HSP72, are used in pharmaceutical
CC compositions, pref. a vaccine, for treating or preventing infection by S.
CC pneumoniae or related bacteria in humans, e.g. S. pyogenes or S.
CC agalactiae
XX
SQ Sequence 352 AA;
Query Match 69.1%; Score 56; DB 2; Length 352;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHGA 12
DB 60 QKRAAYDQYGGAA 71
RESULT 65
ADN26652
ID ADN26652 standard; protein; 362 AA.
XX
AC ADN26652;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #9305.

```

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XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
FN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 9305; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 362 AA;
Query Match 69.1%; Score 56; DB 8; Length 362;
Best Local Similarity 66.7%; Pred. NO. 0.14;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
DB 61 KKKLYDTHGHAAFE 75
RESULT 66
ABU00882

```

Query Match 69.1%; Score 56; DB 6; Length 378;  
Best Local Similarity 91.7%; Pred. No. 0.15;



DT 20-MAY-2004 (first entry)  
 XX Streptococcus pneumoniae protein, Seq ID NO 4647.  
 DE Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.  
 XX Streptococcus pneumoniae.  
 OS US6699703-B1.  
 PN 02-MAR-2004.  
 PD 26-MAY-2000; 2000US-00583110.  
 PF 02-JUL-1997; 97US-0051553P.  
 PR 12-MAY-1998; 98US-0085131P.  
 PR 30-JUN-1998; 98US-00107433.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;  
 PI WPI; 2004-212399/20.  
 DR N-PSDB; ADK45471.  
 DR New nucleic acid molecules and polypeptides useful for diagnosing,  
 PT preventing and treating pathological conditions resulting from bacterial  
 PT infection, e.g. Streptococcus pneumoniae infection, and in drug  
 PT screening.  
 XX Disclosure; SEQ ID NO 4647; 301pp; English.  
 XX The invention relates to isolated Streptococcus pneumoniae nucleic acids  
 CC and polypeptides. The nucleic acids and proteins are useful for  
 CC diagnosing, preventing and treating pathological conditions resulting  
 CC from bacterial infection, such as S. pneumoniae infection. These may also  
 CC be used for drug screening procedures. The present sequence represents a  
 CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence  
 CC data for this patent did not appear in the printed specification but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX SQ Sequence 378 AA;  
 Query Match 69.1%; Score 56; DB 8; Length 378;  
 Best Local Similarity 91.7%; Pred. No. 0.15;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGH 12  
 Db 60 QKRAAYDQYGAA 71  
 RESULT 69  
 ID ABP28852 standard; protein; 379 AA.  
 AC ABP28852;  
 XX 02-JUL-2002 (first entry)  
 DT Streptococcus polypeptide SEQ ID NO 6880.  
 DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX Streptococcus agalactiae.  
 OS WO200234771-A2.  
 PN 02-MAY-2002.  
 PD 02-MAY-2002.  
 PR

PF 29-OCT-2001; 2001WO-GB004789.  
 XX 27-OCT-2000; 2000GB-00026333.  
 PR 24-NOV-2000; 2000GB-00028727.  
 PR 07-MAR-2001; 2001GB-00005640.  
 XX (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;  
 PI Tectelin H;  
 PI WPI; 2002-352536/38.  
 DR N-PSDB; ABN69483.  
 DR New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX Claim 1; Page 3850; 4525pp; English.  
 XX The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71536 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX SQ Sequence 379 AA;  
 Query Match 69.1%; Score 56; DB 5; Length 379;  
 Best Local Similarity 91.7%; Pred. No. 0.15;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGH 12  
 Db 60 QKRAAYDQYGAA 71  
 RESULT 70  
 ID ADR94852 standard; protein; 379 AA.  
 XX ADR94852;  
 AC 16-DEC-2004 (first entry)  
 DT Novel S. pneumoniae protein sequence, SEQ ID 3487.  
 DE Meningitis; bacteraemia; pneumonia; otitis media; vaccine;  
 XX bacterial infection.  
 KW Streptococcus pneumoniae.  
 OS US6800744-B1.  
 PN 05-OCT-2004.  
 XX 30-JUN-1998; 98US-00107433.  
 PF 02-JUL-1997; 97US-0051553P.  
 PR 12-MAY-1998; 98US-0085131P.  
 PR

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XX (GENO-) GENOME THERAPEUTICS CORP.
XX Doucette-Stamm LA, Bush D;
XX
XX WPI: 2004-697205/68.
XX N-PSDB; ADR92249.
XX
XX New isolated nucleic acid encoding a Streptococcus pneumoniae
XX polypeptide, useful for diagnosing, preventing and/or treating
XX pathological conditions resulting from the bacterial infection.
XX
XX Disclosure; SEQ ID NO 3487; 151pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising a sequence
XX encoding a Streptococcus pneumoniae ADR91366polypeptide, or its
XX fragments, with any of 9 fully defined sequences (appearing as ADR94308,
XX ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,
XX ADR96079) or any of the fully defined sequences appearing as ADR91705,
XX ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or
XX ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide
XX sequences, or at least 40, 60 or 300 consecutive nucleotides, which is
XX hybridisable under high stringency conditions to the nucleotide sequence.
XX The nucleic acids and proteins are chosen from 5206 disclosed sequences.
XX Also included are a recombinant expression vector comprising the isolated
XX nucleic acid cited above operably linked to a transcription regulatory
XX element, a cell comprising the recombinant expression vector and a probe
XX comprising at least 20 consecutive nucleotides of the nucleotide
XX sequences as cited above. The methods and compositions of the present
XX invention are useful for the diagnosis, prevention and/or treatment of
XX pathological conditions resulting from bacterial infection by
XX Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and
XX otitis media. The present sequence is one of the 2603 disclosed S.
XX pneumoniae protein sequences. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=6800744B1.
XX
XX Sequence 379 AA;
XX
XX Query Match 69.1%; Score 56; DB 8; Length 379;
XX Best Local Similarity 91.7%; Pred. No. 0.15;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGH 12
XX |||||
XX Db 61 QKRAAYDQYGH 72
XX
XX RESULT 71
XX ABP28853
XX ID ABP28853 standard; protein; 396 AA.
XX AC
XX AC ABP28853;
XX XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Streptococcus polypeptide SEQ ID NO 6882.
XX
XX XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX XX Streptococcus pyogenes.
XX OS
XX XX WO200234771-A2.
XX PN
XX XX 02-MAY-2002.
XX PD
XX XX 29-OCT-2001; 2001WO-GB004789.
XX PF
XX XX 27-OCT-2000; 2000GB-00026333.
XX PR
XX XX 24-NOV-2000; 2000GB-00028727.
XX
XX
XX 07-MAR-2001; 2001GB-00005640.
XX
XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;
XX Tettelin H;
XX
XX WPI; 2002-352536/38.
XX N-PSDB; ABR69484.
XX
XX New Streptococcus protein for the treatment or prevention of infection or
XX disease caused by Streptococcus bacteria, such as meningitis, and for
XX detecting a compound that binds to the protein.
XX
XX Claim 1; Page 3851; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX the specification. The proteins have antibacterial and antiinflammatory
XX activity. (I), nucleic acids encoding (I), ABR66044-ABN71526 and
XX antibodies that bind (I) are used in the manufacture of medicaments for
XX the treatment or prevention of infection or disease caused by
XX Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX Nucleic acids encoding (I) are used to detect Streptococcus in a
XX biological sample. (I) is used to determine whether a compound binds to
XX (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX used as a vaccine or diagnostic composition. The disease caused by
XX Streptococcus that is prevented or treated may be meningitis. Nucleic
XX acid encoding (I) may be used to recombinantly produce (I) and may be
XX used in gene therapy. Antibodies to (I) are used for affinity
XX chromatography, immunoassays, and distinguishing/identifying
XX Streptococcus proteins
XX
XX Sequence 396 AA;
XX
XX Query Match 69.1%; Score 56; DB 5; Length 396;
XX Best Local Similarity 91.7%; Pred. No. 0.16;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGH 12
XX |||||
XX Db 78 QKRAAYDQYGH 89
XX
XX RESULT 72
XX ADL05213
XX ID ADL05213 standard; protein; 407 AA.
XX AC
XX AC ADL05213;
XX XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE M. catarrhalis protein #979.
XX
XX KW Moraxella catarrhalis; infection.
XX
XX OS Moraxella catarrhalis.
XX
XX PN US6673910-B1.
XX XX
XX PD 06-JAN-2004.
XX
XX PF 04-APR-2000; 2000US-00540236.
XX
XX PR 08-APR-1999; 99US-0128416P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL;
XX
XX WPI; 2004-178127/17.
```

DR N-PSDB; ADL03293.

XX New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for

PT preparing a composition for diagnosing, preventing or treating infection

PT caused by Moraxella catarrhalis.

XX

XX Disclosure; SEQ ID NO 2899; 429pp; English.

XX

CC The invention relates to an isolated nucleic acid encoding an Moraxella

CC catarrhalis polypeptide. The nucleic acid is useful for preparing a

CC composition for diagnosing, preventing or treating infection caused by

CC Moraxella catarrhalis. The present sequence represents the amino acid

CC sequence of a M. catarrhalis protein.

XX

XX Sequence 407 AA;

XX

Query Match 69.1%; Score 56; DB 8; Length 407;

Best Local Similarity 60.0%; Pred. No. 0.16;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0

Qy 1 OKRAAYDQYGHAAFE 15

Db 84 EKRATYDRMGHSAVE 98

||| ||: ||: ||

RESULT 73

AAB05934

ID AAB05934 standard; protein; 368 AA.

XX

AC AAB05934;

XX

XX 20-OCT-2000 (first entry)

XX

DE Protein deduced from Mycoplasma hyopneumoniae genomic clone pAD612.

XX

XX Mycoplasma hyopneumoniae; vaccine; antigen; antimicrobial;

KW enzootic pneumonia.

XX

OS Mycoplasma hyopneumoniae.

XX

XX W0200031115-A1.

XX

XX 02-JUN-2000.

XX

XX 19-NOV-1999; 99WO-AU001035.

XX

XX 20-NOV-1998; 98AU-00007273.

XX

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA

XX Moore RJ, Doran TJ;

PI

XX WPI; 2000-400031/34.

DR

XX N-PSDB; AAA56820.

XX

XX Identifying antigenic polypeptides for use in vaccines against Mycoplasma

PT infection comprises screening proteins co-expressed with a marker.

XX

XX Claim 27; Fig 1; 241pp; English.

XX

XX The present sequence is encoded by a clone selected from a Mycoplasma

XX hyopneumoniae genomic DNA library. M. hyopneumoniae causes Enzootic

CC pneumonia in pigs. The infection rarely causes death but often results in

CC significant depression, leading to reduced weight gain. The animals are

CC also prone to secondary infection by opportunistic pathogens. Genomic DNA

CC from M. hyopneumoniae was partially digested with restriction enzymes and

CC fragments were ligated downstream of the polyHis tag region in the

CC expression vector pCI. The ligation mixture was used to transform

CC competent E. coli cells and polyHis positive clones were selected using

CC anti-polyHis antibodies. Expression of the recombinant vector generates

CC PolyHis fusion proteins which are easily identified and isolated. Pigs

CC were vaccinated with plasmid DNA from polyHis positive clones in order to

CC identify clones encoding antigenic proteins which confer protection

## RESULT 75

ABR55123  
ID ABR55123 standard; peptide; 15 AA.

XX AC ABR55123;

XX DT 03-JUL-2003 (first entry)

XX DE E. coli dnaJp2 antigen-specific epitope peptide.

XX KW Antigen-specific epitope; immune response; T cell; cytokine;  
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;  
KW cytostatic; antithyroid; anti-asthmatic; immunosuppressive;  
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;  
KW antiallergic; dermatological; antipsoriatic.

XX OS Escherichia coli.

XX PN WO2003026579-A2.

XX PD 03-APR-2003.

XX PF 25-SEP-2002; 2002WO-US030578.

XX PR 25-SEP-2001; 2001US-0325499P.

XX PR 11-DEC-2001; 2001US-0339284P.

XX XX (REGC ) UNIV CALIFORNIA.

XX PA Alhani S, Martins A;

XX PI WPI; 2003-430097/40.

XX PT Modulating an immune response in a subject having an immune-related  
PT disorder, e.g. arthritis by administering an antigen-specific epitope and  
PT a cytokine or an agent that effects cytokine activity or expression.

XX PS Disclosure; Page 9; 41pp; English.

XX CC The invention relates to a novel method for modulating an immune response  
CC in a subject having an immune-related disorder. The method comprises: (a)  
CC administering an antigen-specific epitope, where administration provides  
CC epitope-specific T cell immune modulation; and (b) administering a  
CC cytokine, an agent that effects cytokine activity or expression, or an  
CC anticytokine therapy. The method of the invention has antiarthritic,  
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,  
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-  
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,  
CC dermatological, and antipsoriatic activity. The method is useful for  
CC modulating an immune response in a subject having an immune-related  
CC disorder. The present sequence is used in the exemplification of the  
CC invention

XX SQ Sequence 15 AA;

Query Match 66.7%; Score 54; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10

Db 6 QKRAAYDQYG 15

## RESULT 76

AAG48466  
ID AAG48466 standard; protein; 332 AA.

XX AC AAG48466;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 61205.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX TN 06-SEP-2000.  
XX PD 25-FEB-2000; 2000EP-00301439.  
XX PF 25-FEB-1999; 99US-0121825P.  
XX PR 05-MAR-1999; 99US-0123180P.  
XX PR 09-MAR-1999; 99US-0123548P.  
XX PR 23-MAR-1999; 99US-0125788P.  
XX PR 25-MAR-1999; 99US-0126284P.  
XX PR 29-MAR-1999; 99US-0126785P.  
XX PR 01-APR-1999; 99US-0127462P.  
XX PR 06-APR-1999; 99US-0128234P.  
XX PR 08-APR-1999; 99US-0128714P.  
XX PR 16-APR-1999; 99US-0129845P.  
XX PR 19-APR-1999; 99US-0130077P.  
XX PR 21-APR-1999; 99US-0130449P.  
XX PR 23-APR-1999; 99US-0130510P.  
XX PR 23-APR-1999; 99US-0130891P.  
XX PR 28-APR-1999; 99US-0131449P.  
XX PR 30-APR-1999; 99US-0132048P.  
XX PR 30-APR-1999; 99US-0132407P.  
XX PR 04-MAY-1999; 99US-0132484P.  
XX PR 05-MAY-1999; 99US-0132485P.  
XX PR 06-MAY-1999; 99US-0132486P.  
XX PR 06-MAY-1999; 99US-0132487P.  
XX PR 07-MAY-1999; 99US-0132863P.  
XX PR 11-MAY-1999; 99US-0134256P.  
XX PR 14-MAY-1999; 99US-0134218P.  
XX PR 14-MAY-1999; 99US-0134219P.  
XX PR 14-MAY-1999; 99US-0134221P.  
XX PR 14-MAY-1999; 99US-0134370P.  
XX PR 18-MAY-1999; 99US-0134768P.  
XX PR 19-MAY-1999; 99US-0134941P.  
XX PR 20-MAY-1999; 99US-0135124P.  
XX PR 21-MAY-1999; 99US-0135353P.  
XX PR 24-MAY-1999; 99US-0135629P.  
XX PR 25-MAY-1999; 99US-0136021P.  
XX PR 27-MAY-1999; 99US-0136392P.  
XX PR 28-MAY-1999; 99US-0136782P.  
XX PR 01-JUN-1999; 99US-0137222P.  
XX PR 03-JUN-1999; 99US-0137528P.  
XX PR 04-JUN-1999; 99US-0137502P.  
XX PR 07-JUN-1999; 99US-0137724P.  
XX PR 08-JUN-1999; 99US-0138094P.  
XX PR 10-JUN-1999; 99US-0138540P.  
XX PR 10-JUN-1999; 99US-0138847P.  
XX PR 14-JUN-1999; 99US-0139119P.  
XX PR 16-JUN-1999; 99US-0139452P.  
XX PR 16-JUN-1999; 99US-0139453P.  
XX PR 17-JUN-1999; 99US-0139492P.  
XX PR 18-JUN-1999; 99US-0139454P.  
XX PR 18-JUN-1999; 99US-0139455P.  
XX PR 18-JUN-1999; 99US-0139456P.  
XX PR 18-JUN-1999; 99US-0139457P.  
XX PR 18-JUN-1999; 99US-0139458P.  
XX PR 18-JUN-1999; 99US-0139459P.  
XX PR 18-JUN-1999; 99US-0139460P.  
XX PR 18-JUN-1999; 99US-0139461P.  
XX PR 18-JUN-1999; 99US-0139462P.  
XX PR 18-JUN-1999; 99US-0139463P.  
XX PR 18-JUN-1999; 99US-0139750P.  
XX PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999;	99US-0139817P.
PR 22-JUN-1999;	99US-0139899P.
PR 23-JUN-1999;	99US-0140353P.
PR 23-JUN-1999;	99US-0140354P.
PR 24-JUN-1999;	99US-0140695P.
PR 28-JUN-1999;	99US-0140823P.
PR 29-JUN-1999;	99US-0140991P.
PR 30-JUN-1999;	99US-0141287P.
PR 01-JUL-1999;	99US-0141842P.
PR 01-JUL-1999;	99US-0142154P.
PR 02-JUL-1999;	99US-0142055P.
PR 06-JUL-1999;	99US-0142390P.
PR 08-JUL-1999;	99US-0142803P.
PR 09-JUL-1999;	99US-0142970P.
PR 12-JUL-1999;	99US-0142977P.
PR 13-JUL-1999;	99US-0143542P.
PR 14-JUL-1999;	99US-0143624P.
PR 15-JUL-1999;	99US-0144005P.
PR 16-JUL-1999;	99US-0144085P.
PR 16-JUL-1999;	99US-0144086P.
PR 19-JUL-1999;	99US-0144325P.
PR 19-JUL-1999;	99US-0144331P.
PR 19-JUL-1999;	99US-0144332P.
PR 19-JUL-1999;	99US-0144333P.
PR 19-JUL-1999;	99US-0144334P.
PR 19-JUL-1999;	99US-0144335P.
PR 20-JUL-1999;	99US-0144352P.
PR 20-JUL-1999;	99US-0144632P.
PR 20-JUL-1999;	99US-0144884P.
PR 21-JUL-1999;	99US-0144814P.
PR 21-JUL-1999;	99US-0145086P.
PR 21-JUL-1999;	99US-0145088P.
PR 22-JUL-1999;	99US-0145085P.
PR 22-JUL-1999;	99US-0145087P.
PR 22-JUL-1999;	99US-0145089P.
PR 22-JUL-1999;	99US-0145152P.
PR 23-JUL-1999;	99US-0145145P.
PR 23-JUL-1999;	99US-0145218P.
PR 23-JUL-1999;	99US-0145224P.
PR 26-JUL-1999;	99US-0145276P.
PR 27-JUL-1999;	99US-0145913P.
PR 27-JUL-1999;	99US-0145918P.
PR 27-JUL-1999;	99US-0145919P.
PR 28-JUL-1999;	99US-0145951P.
PR 02-AUG-1999;	99US-0146386P.
PR 02-AUG-1999;	99US-0146388P.
PR 02-AUG-1999;	99US-0146389P.
PR 03-AUG-1999;	99US-0147038P.
PR 04-AUG-1999;	99US-0147204P.
PR 04-AUG-1999;	99US-0147302P.
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PR 16-SEP-1999;	99US-0154039P.
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PR 23-SEP-1999;	99US-0155486P.
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PR 29-OCT-1999;	99US-0162142P.
Query Match 66.7%; Score 54; DB 3; Length 332;	
Best Local Similarity 66.7%; Pred. No. 0.3;	
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
QY	1 QKRAAYDQYGHAAFE 15
Db	26 EKRDLYDQVGHEAFE 40
RESULT 77	
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ID AAG48465 standard; protein; 367 AA.	
XX AC AAG48465;	
XX DT 18-OCT-2000 (first entry)	
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 61204.	
XX KW Protein identification; signal transduction pathway; metabolic pathway;	
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;	
XX KW termination sequence.	

OS	Arabidopsis thaliana.		
XX	EP1033405-A2.	PR	30-JUN-1999;
XX		PR	01-JUL-1999;
XX		PR	01-JUL-1999;
XX		PR	02-JUL-1999;
PD		PR	06-JUL-1999;
XX	06-SEP-2000.	PR	08-JUL-1999;
XX		PR	09-JUL-1999;
XX	25-FEB-2000; 2000EP-00301439.	PR	12-JUL-1999;
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XX		PR	15-JUL-1999;
PR	25-FEB-1999;	PR	16-JUL-1999;
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 PR 24-SEP-1999; 99US-0155569P.  
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 PR 29-SEP-1999; 99US-0156536P.  
 PR 04-OCT-1999; 99US-0157117P.  
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 PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 54; DB 3; Length 367;  
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 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
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 Db 61 EKRDLYDQVGHEAPE 75

RESULT 78  
 AAY34469  
 ID AAY34469 standard; protein; 383 AA.

XX AC AAY34469;  
 XX DT 27-AUG-2003 (revised)  
 DT 20-MAR-2003 (revised)  
 DT 25-AUG-1999 (first entry)  
 XX XX  
 DE Porphyromonas gingivalis protein PG124.  
 XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;  
 KW antigenic.  
 XX Porphyromonas gingivalis.  
 OS  
 XX WO9929870-A1.  
 PN  
 XX 17-JUN-1999.  
 PD  
 XX

PF 10-DEC-1998; 98WO-AU001023.  
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 PR 10-DEC-1997; 97AU-00000839.  
 PR 31-DEC-1997; 97AU-00001182.  
 PR 30-JAN-1998; 98AU-00001546.  
 PR 10-MAR-1998; 98AU-00002264.  
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 PR 05-MAY-1998; 98AU-00003338.  
 PR 22-MAY-1998; 98AU-00003654.  
 PR 29-JUL-1998; 98AU-00004917.  
 PR 30-JUL-1998; 98AU-00004963.  
 PR 04-AUG-1998; 98AU-00005028.  
 XX  
 PA (CSLC-) CSL LTD.  
 XX  
 PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;  
 PI Hocking DM, Webb EA;  
 XX  
 DR WPI; 1999-385613/32.  
 DR N-PSDB; AAX91687.  
 XX  
 PT Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.  
 XX  
 PS Claim 1; Page 447-448; 588pp; English.  
 XX  
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic  
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to  
 CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the  
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial  
 CC activity with a vaccine mechanism of action. The PG polypeptides can be  
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can  
 CC be used to detect Porphyromonas gingivalis in standard hybridisation  
 CC assays. Porphyromonas gingivalis is involved in periodontal disease  
 CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)  
 CC (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 383 AA;  
 Query Match 66.7%; Score 54; DB 2; Length 383;  
 Best Local Similarity 75.0%; Pred. No. 0.35;  
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 QY 1 QKRAAYDQYGHGA 12  
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 RESULT 79  
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 ID AAY34345 standard; protein; 384 AA.  
 XX  
 AC AAY34345;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 20-MAR-2003 (revised)  
 DT 25-AUG-1999 (first entry)  
 XX XX  
 DE Porphyromonas gingivalis protein PG124.  
 XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;  
 KW antigenic.  
 XX Porphyromonas gingivalis.  
 OS  
 XX WO9929870-A1.  
 PN  
 XX 17-JUN-1999.  
 PD  
 XX  
 PF 10-DEC-1998; 98WO-AU001023.  
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 PR 10-DEC-1997; 97AU-00000839.  
 PR 31-DEC-1997; 97AU-00001182.









XX	(GENO-) GENOME THERAPEUTICS CORP.
PA	
XX	Breton G, Bush D;
XX	
XX	WPI: 2003-576092/54.
DR	N-PSDB; ADA29571.
XX	
XX	New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT	for diagnosing a bacterial disease, as components of antibacterial
PT	vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT	plants.
XX	
XX	Example; SEQ ID NO 4984; 328pp; English.
PS	
XX	
XX	The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC	The A. baumannii nucleic acids and polypeptides are useful as reagents
CC	for diagnosing a bacterial disease, as components of antibacterial
CC	vaccines, as targets for antibacterial drugs, to detect the presence of
CC	A. baumannii and other Acinetobacter species in a sample, in screening
CC	compounds for the ability to interfere with the A. baumannii life cycle
CC	or to inhibit A. baumannii infection, and as biocontrol agents for
CC	plants. The present sequence represents the amino acid sequence of an A.
CC	baumannii protein.
XX	
XX	Sequence 375 AA;
SS	
XX	Query Match 64.2%; Score 52; DB 6; Length 375;
CC	Best Local Similarity 60.0%; Pred. No. 0.78;
CC	Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0
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QY	1 QKRAAYDQYGHAAFE 15
	:  :   :
Db	66 EKRSMDYDRMGHNAFE 80
RESULT 84	
ADN18559	
ID	ADN18559 standard; protein; 376 AA.
XX	
AC	ADN18559;
XX	
DT	02-DEC-2004 (first entry)
XX	
XX	Bacterial polypeptide #1212.
XX	
XX	Recombinant DNA construct; transformed plant; improved plant property;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW	pathogen tolerance; pest tolerance; plant disease resistance;
KW	cell cycle pathway modification; plant growth regulator;
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW	bacterial polypeptide.
XX	
OS	Bacteria.
XX	
XX	US2003233675-A1.
PN	
XX	
PD	18-DEC-2003.
XX	
XX	20-FEB-2003; 2003US-00369493.
PF	
XX	
XX	21-FEB-2002; 2002US-0360039P.
PR	
XX	
PA	(CAOY/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
XX	
XX	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI	
XX	WPI: 2004-061375/06.
DR	

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XX WPI; 2003-029926/02.
DR N-PSDB; ACA30497.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 54551; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: the sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 297 AA;

Query Match 61.7%; Score 50; DB 6; Length 297;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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DB 58 KKRAQYDQYGSWF 71

RESULT 86
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AC AAG30655;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 36688.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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Query Match 61.7%; Score 50; DB 3; Length 320;

Best Local Similarity 90.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10

DB 33 QKRAVVDQYG 42

RESULT 87

AAG30654

ID AAG30654 standard; protein; 348 AA.

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AC AAG30654;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 36687.

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KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

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PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-00301439.

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Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 61 QKRAAYDQYG 70

RESULT 88
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ID ABM70982 standard; protein; 379 AA.
XX AC ABM70982;
XX DT 20-NOV-2003 (first entry)
XX DE Staphylococcus aureus protein #222.
XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX KW enzymatic assay; antibiotic target.
XX OS Staphylococcus aureus.
XX PN W0200294868-A2.
XX PD 28-NOV-2002.
XX PF 27-MAR-2002; 2002WO-IB002637.
XX PR 27-MAR-2001; 2001GB-00007661.
XX PA (CHIR-) CHIRON SPA.
XX DI Masignani V, Mora M, Scarselli M;
XX WPI; 2003-120786/11.
XX DR N-PSDB; ACF72542.
XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or
XX PT preventing Staphylococcal infection, specifically an infection caused by
XX PT S. aureus, e.g. sepsis.

PS Claim 1; SEQ ID NO 444; 49pp; English.
XX CC The invention relates to novel genes and encoded proteins from
XX CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX CC nucleic acid encoding the protein, or an antibody to the protein, is
XX CC useful as a pharmaceutical, particularly as a vaccine for treating or
XX CC preventing infection due to Staphylococcus bacteria, specifically an
XX CC infection caused by S. aureus. The composition is particularly useful for
XX CC treating or preventing sepsis in a patient. The composition can also be
XX CC used for diagnostics. The protein is also used in an assay for enzymatic
XX CC studies and as a target for antibiotics. This sequence represents one of
XX CC the novel S. aureus proteins of the invention
XX SQ Sequence 379 AA;

Query Match 61.7%; Score 50; DB 6; Length 379;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 11
Db 61 KRAAYDQYGH 70

RESULT 89
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ID AAG53768 standard; protein; 295 AA.
XX AC AAG53768;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 68486.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
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XX PR 29-MAR-1999; 99US-0126785P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match      60.5%; Score 49; DB 3; Length 295;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10
Db 33 QKRAIYDQYG 42

RESULT 90
AAG18158
ID AAG18158 standard; protein; 295 AA.
XX AC AAG18158;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 19453.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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Query Match 60.5%; Score 49; DB 3; Length 350;  
Best Local Similarity 90.0%; Pred. No. 2.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
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Db 88 QKRAIYDQYG 97

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AC AAG18156;  
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DI 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19451.  
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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
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XX  
PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-00301439.  
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Query Match 60.5%; Score 49; DB 3; Length 350;
Best Local Similarity 90.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
Db 88 QKRAAYDQYG 97
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RESULT 95
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AC ADS28176;
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DT 02-DEC-2004 (first entry)
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DE Bacterial polypeptide #17209.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX

OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
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PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 17209; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 370 AA;

Query Match 60.5%; Score 49; DB 8; Length 370;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 60 QKRAHYDQFGH 70
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RESULT 96
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AC ADS23586;
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DT 02-DEC-2004 (first entry)
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DE Bacterial polypeptide #12619.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
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PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
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Query Match 58.0%; Score 47; DB 3; Length 309;

Best Local Similarity 80.0%; Pred. No. 5.1;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 100

AAG16066

ID AAG16066 standard; protein; 337 AA.

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DT 17-OCT-2000 (first entry)

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 16564.

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KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

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XX 25-FEB-2000; 2000EP-00301439.

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Query Match 58.0%; Score 47; DB 3; Length 337;  
Best Local Similarity 80.0%; Pred. No. 5.6;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
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Db 61 QKXAVDQYG 70

Search completed: September 2, 2005, 20:55:22  
Job time : 170 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: September 2, 2005, 20:48:42 ; Search time 22 Seconds  
(without alignments)  
50.897 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

## Database :

Issued Patents AA:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	81	100.0	15	3	US-09-107-615-4
3	81	100.0	15	4	US-09-756-983-10
4	81	100.0	15	5	PCT-US95-04896-4
5	81	100.0	131	3	US-09-553-498-4
6	81	100.0	131	4	US-09-618-869-4
7	81	100.0	380	4	US-09-543-681A-5912
8	81	100.0	380	4	US-09-489-039A-9011
9	81	100.0	399	3	US-09-553-498-2
10	81	100.0	399	4	US-08-618-869-2
11	72	88.9	15	1	US-08-618-464-5
12	72	88.9	15	3	US-09-107-615-5
13	72	88.9	15	5	PCT-US95-04896-5
14	62	76.5	381	4	US-09-252-991A-27174
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16	56	69.1	378	4	US-09-583-110-4647
17	56	69.1	379	4	US-09-107-433-3487
18	56	69.1	407	4	US-09-540-236-2899
19	55	67.9	368	4	US-08-618-464-2
20	54	66.7	15	1	US-08-618-464-6
21	54	66.7	15	3	US-09-107-615-6
22	53	65.4	240	4	US-09-248-796A-17703
23	52	64.2	375	4	US-09-328-352-4984
24	47	58.0	138	4	US-09-902-540-13689
25	47	58.0	373	4	US-09-710-279-890
26	47	58.0	385	3	US-09-134-001C-3688
27	44	54.3	387	4	US-09-908-992B-11

28	44	54.3	397	4	US-09-248-796A-17628	Sequence 17628, A
29	44	54.3	414	4	US-09-908-992B-10	Sequence 10, Appl
30	44	54.3	419	2	US-08-686-417-3	Sequence 3, Appli
31	44	54.3	452	4	US-09-908-992B-29	Sequence 29, Appl
32	44	54.3	453	4	US-09-908-992B-9	Sequence 9, Appli
33	44	54.3	479	4	US-09-908-992B-30	Sequence 30, Appl
34	44	54.3	479	4	US-09-908-992B-28	Sequence 28, Appl
35	44	54.3	480	4	US-09-908-992B-8	Sequence 8, Appli
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56	38	46.9	108	3	US-09-113-977C-38	Sequence 38, Appl
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62	38	46.9	108	4	US-09-351-048A-38	Sequence 38, Appl
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96	36	44.4	337	4	US-09-665-479A-8	Sequence 8, Appli
97	36	44.4	387	4	US-09-489-039A-10623	Sequence 10623, A
98	36	44.4	412	4	US-09-252-991A-26237	Sequence 26237, A
99	36	44.4	487	4	US-09-252-991A-21980	Sequence 21980, A
100	36	44.4				

## ALIGNMENTS

```
RESULT 1
US-08-618-464-4
; Sequence 4, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: INVOLVED IN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-4

Query Match 100.0%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 2
US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
```

```
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-4

Query Match 100.0%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
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;  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5912  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5912

Query Match 100.0%; Score 81; DB 4; Length 380;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 63 QKRAAYDQYGHAAFE 77  
|||||

RESULT 8  
US-09-489-039A-9011  
; Sequence 9011, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 9011  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9011

Query Match 100.0%; Score 81; DB 4; Length 380;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 64 QKRAAYDQYGHAAFE 78  
|||||

RESULT 9  
US-09-553-498-2  
; Sequence 2, Application US/09553498  
; Patent No. 6309861  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorothee  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote  
; FILE REFERENCE: Case 20379  
; CURRENT APPLICATION NUMBER: US/09/553,498  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: EP9107412.1  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 2  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: E. coli  
US-09-553-498-2

Query Match 100.0%; Score 81; DB 3; Length 399;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 84 QKRAAYDQYGHAAFE 98  
|||||

RESULT 10  
US-09-618-869-2  
; Sequence 2, Application US/09618869  
; Patent No. 6455279  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorothee  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR  
; TITLE OF INVENTION: CHAPERONES  
; FILE REFERENCE: 20381  
; CURRENT APPLICATION NUMBER: US/09/618,869  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: EP99114811.5  
; PRIOR FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-618-869-2

Query Match 100.0%; Score 81; DB 4; Length 399;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 84 QKRAAYDQYGHAAFE 98  
|||||

RESULT 11  
US-08-618-464-5  
; Sequence 5, Application US/08618464  
; Patent No. 5773570  
; GENERAL INFORMATION:  
; APPLICANT: CARSON, DENNIS A.  
; APPLICANT: ALBANI, SALVATORE  
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
; TITLE OF INVENTION: INDUCING  
; TITLE OF INVENTION: INVOLVED IN  
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FISH & RICHARDSON P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/618,464  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOWELLS, STACY L.  
; REGISTRATION NUMBER: 34,842  
; REFERENCE/DOCKET NUMBER: 07340/042001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: Immunogenic dnaJ Peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..15  
US-08-618-464-5

Query Match 88.9%; Score 72; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.2e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||  
Db 2 ERAAYDQYGHAAFE 15

## RESULT 12

US-09-107-615-5  
Sequence 5, Application US/09107615  
Patent No. 6153200

GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.  
APPLICANT: ALBANI, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
INDUCING IMMUNE PROTECTION AGAINST  
TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN  
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,615  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,464  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOWELLS, STACY L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/042001  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: Immunogenic dnaJ Peptide  
FEATURE:  
NAME/KEY: Peptide

LOCATION: 1..15  
US-09-107-615-5

Query Match 88.9%; Score 72; DB 3; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.2e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||  
Db 2 ERAAYDQYGHAAFE 15

## RESULT 13

PCT-US95-04896-5  
Sequence 5, Application PC/TUS9504896

GENERAL INFORMATION:  
APPLICANT: THE REGENTS OF THE UNIVERSITY  
OF CALIFORNIA  
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT  
OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBBINS, BERLINER & CARSON  
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04896  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: BERLINER, ROBERT  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-314  
TELEPHONE: 213-977-1001  
TELEFAX: 213-977-1003

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: Immunogenic dnaJ Peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..15  
PCT-US95-04896-5

Query Match 88.9%; Score 72; DB 5; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.2e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||  
Db 2 ERAAYDQYGHAAFE 15

## RESULT 14

US-09-252-991A-27174  
Sequence 27174, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27174
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27174

Query Match 76.5%; Score 62; DB 4; Length 381;
Best Local Similarity 78.6%; Pred. No. 0.0041;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
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Db 66 KRAAYDQYGHAGVD 79

RESULT 15
US-08-472-534-6
; Sequence 6, Application US/08472534
; Patent No. 5919620
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,534
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Biovac-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-534-6

Query Match 69.1%; Score 56; DB 2; Length 352;
Best Local Similarity 91.7%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
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Db 60 QKRAAYDQYGHGA 71
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US-09-583-110-4647
; Sequence 4647, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4647
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4647

Query Match 69.1%; Score 56; DB 4; Length 378;
Best Local Similarity 91.7%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12
|||||
Db 60 QKRAAYDQYGHGA 71

RESULT 17
US-09-107-433-3487
; Sequence 3487, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
```

TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 3487:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...379  
SEQUENCE DESCRIPTION: SEQ ID NO: 3487:  
US-09-107-433-3487

Query Match 69.1%; Score 56; DB 4; Length 379;  
Best Local Similarity 91.7%; Pred. No. 0.048;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12  
DB 61 QKRAAYDQYGHGA 72

RESULT 18  
US-09-540-236-2899  
Sequence 2899, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 2899  
LENGTH: 407  
TYPE: PRT  
ORGANISM: M.catarrhalis  
US-09-540-236-2899

Query Match 69.1%; Score 56; DB 4; Length 407;  
Best Local Similarity 60.0%; Pred. No. 0.052;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
DB 84 EKRATYDRMGHSAYE 98

RESULT 19  
US-09-861-451A-2  
Sequence 2, Application US/09861451A  
Patent No. 6759516  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific & Industrial Research Orga  
TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences  
FILE REFERENCE: FP3403701  
CURRENT APPLICATION NUMBER: US/09/861,451A  
CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: PF7273  
PRIOR FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 2  
LENGTH: 368  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Deduced protein  
OTHER INFORMATION: sequence from clone PAD612

US-09-861-451A-2

Query Match 67.9%; Score 55; DB 4; Length 368;  
Best Local Similarity 64.3%; Pred. No. 0.07;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAPE 15  
DB 67 KRQYDKFGHAAFD 80

RESULT 20  
US-08-618-464-6  
Sequence 6, Application US/08618464  
Patent No. 5773570  
GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.  
TITLE OF INVENTION: ALBANT, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
TITLE OF INVENTION: INDUCING  
TITLE OF INVENTION: INVOLVED IN  
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,464  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: HOWELLS, STACY L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/042001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: dnaJp2  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1...15  
US-08-618-464-6

Query Match 66.7%; Score 54; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
DB 6 QKRAAYDQYG 15

RESULT 21  
US-09-107-615-6  
Sequence 6, Application US/09107615  
Patent No. 6153200

GENERAL INFORMATION:  
; APPLICANT: CARSON, DENNIS A.  
; APPLICANT: ALBANI, SALVATORE  
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
; INDUCING IMMUNE PROTECTION AGAINST  
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN  
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & RICHARDSON P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,615  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/618,464  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOWELLS, STACY L.  
; REGISTRATION NUMBER: 34,842  
; REFERENCE/DOCKET NUMBER: 07340/042001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: dnaJp2  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..15  
US-09-107-615-6

Query Match 66.7%; Score 54; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
Db 6 QKRAAYDQYG 15

RESULT 22  
US-09-248-796A-17703  
; Sequence 17703, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17703  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-17703

Query Match 65.4%; Score 53; DB 4; Length 240;  
Best Local Similarity 60.0%; Pred. No. 0.1; Mismatches 4; Indels 2; Gaps 0;  
Matches 9; Conservative 4; Mismatches 4; Indels 2; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
Db 104 EKRAAYDQFGASAFD 118

RESULT 23  
US-09-328-352-4984  
; Sequence 4984, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4984  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (322)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown  
US-09-328-352-4984

Query Match 64.2%; Score 52; DB 4; Length 375;  
Best Local Similarity 60.0%; Pred. No. 0.24; Mismatches 3; Indels 3; Gaps 0;  
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
Db 66 EKRSWYDMGHNAFE 80

RESULT 24  
US-09-902-540-13689  
; Sequence 13689, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13689  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13689

Query Match 58.0%; Score 47; DB 4; Length 138;  
Best Local Similarity 58.3%; Pred. No. 0.65; Mismatches 4; Indels 1; Gaps 0;  
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGHGA 12



Db           ::||| ||:||||  
66 ERRARYDRFGHA 77

## RESULT 25

US-09-710-279-890  
; Sequence 890, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 890  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-890

Query Match           58.0%; Score 47; DB 4; Length 373;  
Best Local Similarity   80.0%; Pred. No. 1.9;  
Matches   8; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy           2 KRAAYDQVGH 11  
             ||| |||:||||  
Db           61 KRAYDQFGH 70

## RESULT 26

US-09-134-001C-3688  
; Sequence 3688, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3688  
; LENGTH: 385  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3688

Query Match           58.0%; Score 47; DB 3; Length 385;  
Best Local Similarity   80.0%; Pred. No. 1.9;  
Matches   8; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy           2 KRAAYDQVGH 11  
             ||| |||:||||  
Db           73 KRAYDQFGH 82

## RESULT 27

US-09-908-992B-11  
; Sequence 11, Application US/09908992B  
; Patent No. 6825005  
; GENERAL INFORMATION:  
; APPLICANT: SYKEN, JOSH

; APPLICANT: MUNGER, KARL  
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS  
; FILE REFERENCE: HMV-054.01  
; CURRENT APPLICATION NUMBER: US/09/908,992B  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/219,718  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/219,537  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-908-992B-11

Query Match           54.3%; Score 44; DB 4; Length 387;  
Best Local Similarity   57.1%; Pred. No. 6.7;  
Matches   8; Conservative   1; Mismatches   5; Indels   0; Gaps   0;

Qy           2 KRAAYDQYGHAAPE 15  
             ||| |||:||||  
Db           84 KRQYDAYGSAGFD 97

## RESULT 28

US-09-248-796A-17628  
; Sequence 17628, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17628  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-17628

Query Match           54.3%; Score 44; DB 4; Length 397;  
Best Local Similarity   80.0%; Pred. No. 6.8;  
Matches   8; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy           1 QKRAAYDQYG 10  
             ||| |||:||||  
Db           65 QKREIYDQYG 74

## RESULT 29

US-09-908-992B-10  
; Sequence 10, Application US/09908992B  
; Patent No. 6825005  
; GENERAL INFORMATION:  
; APPLICANT: SYKEN, JOSH  
; APPLICANT: MUNGER, KARL  
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS  
; FILE REFERENCE: HMV-054.01  
; CURRENT APPLICATION NUMBER: US/09/908,992B  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/219,718  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/219,537  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 30

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-10

Query Match      54.3%; Score 44; DB 4; Length 414;
Best Local Similarity 57.1%; Pred. No. 7.1;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      84 KRQYDAYGSAGFD 97

RESULT 30
US-08-686-417-3
; Sequence 3, Application US/08686417
; Patent No. 5850018
; GENERAL INFORMATION:
; APPLICANT: Baczynski, Chris
; APPLICANT: Barbour, Eric
; APPLICANT: Horowitz, Jeannine
; APPLICANT: Rosichan, Jeffrey L.
; TITLE OF INVENTION: AN EXPRESSION CONTROL SEQUENCE FOR
; TITLE OF INVENTION: GENERAL AND EFFECTIVE EXPRESSION OF GENES IN PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,417
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 27112-20038.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-686-417-3

Query Match      54.3%; Score 44; DB 2; Length 419;
Best Local Similarity 53.3%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KRAAYDQYGHAAFE 15
Db      65 EKREIYDQGEDALK 79

RESULT 31
US-09-908-992B-29
; Sequence 29, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Mus sp.
; NAME/KEY: MOD RES
; LOCATION: (206)..(224)
; OTHER INFORMATION: Unknown amino acid
US-09-908-992B-29

Query Match      54.3%; Score 44; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 7.8;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      150 KRQYDAYGSAGFD 163

RESULT 32
US-09-908-992B-9
; Sequence 9, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-9

Query Match      54.3%; Score 44; DB 4; Length 453;
Best Local Similarity 57.1%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      150 KRQYDAYGSAGFD 163

RESULT 33
US-09-908-992B-30
; Sequence 30, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
```

```

; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-908-992B-30

```

Query Match 54.3%; Score 44; DB 4; Length 453;  
Best Local Similarity 57.1%; Pred. No. 7.9;  
Matches 8; Conservative 1; Mismatches 5; Indels

```

RESULT 34
US-09-908-992B-28
; Sequence 28, Application US/09908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN, JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (206)..(224)
; OTHER INFORMATION: Unknown amino acid
US-09-908-992B-28

```

Query Match 54.3%; Score 44; DB 4; Length 479;  
Best Local Similarity 57.1%; Pred. NO. 8.3;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 35  
US-09-908-992B-8  
; Sequence 8, Application US/0908992B  
; Patent No. 6825005  
; GENERAL INFORMATION:  
; APPLICANT: SYKEN, JOSH  
; APPLICANT: MUNGER, KARL  
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS  
; FILE REFERENCE: HMV-054.01  
; CURRENT APPLICATION NUMBER: US/09/908,992B  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/219,718  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/219,537  
; PRIOR FILING DATE: 2000-07-20

```

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 480
; TYPE: prt
; ORGANISM: Homo sapiens
US-9-908-992B-8

```

Query Match 54.3%; Score 44; DB 4; Length 480;  
Best Local Similarity 57.1%; Pred. No. 8.4;  
Matches 8; Conservative 1; Mismatches 5; Indels

```

RESULT 36
US-09-908-992B-12
US-09-908-992B-12, Application US/0908992B
; Sequence 12, Application US/0908992B
; Patent No. 6825005
; GENERAL INFORMATION:
; APPLICANT: SYKEN JOSH
; APPLICANT: MUNGER, KARL
; TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
; FILE REFERENCE: HMV-054.01
; CURRENT APPLICATION NUMBER: US/09/908,992B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,718
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/219,537
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-992B-12

```

Query Match 54.3%; Score 44; DB 4; Length 480;  
Best Local Similarity 57.1%; Pred. No. 8.4;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

RESULT 37
US-09-882-835-4
; Sequence 4, Application US/09882835
; Patent No. 6462187
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22109, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-063001
; CURRENT APPLICATION NUMBER: US/09/882,835
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,673
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; - LENGTH: 87
; - TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-882-835-4
Query Match          50.6%;      Score 41;      DB 4;      Length 87;

```

Best Local Similarity 77.8%; Pred. No. 4.7;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10  
:|||||  
Db 79 RRAAYDQYG 87

RESULT 38  
US-09-658-644-4  
; Sequence 4, Application US/09658644  
; Patent No. 6537554  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Jeffers, Michael  
; TITLE OF INVENTION: Nucleotide Sequences and Amino Acid Sequences of  
; TITLE OF INVENTION: Secreted Proteins Involved in Angiogenesis  
; FILE REFERENCE: 15966-S17 CIP1  
; CURRENT APPLICATION NUMBER: US/09/658,644  
; CURRENT FILING DATE: 2001-09-09  
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/150,684  
; PRIOR FILING DATE: 1998-09-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-658-644-4

Query Match 50.6%; Score 41; DB 4; Length 223;  
Best Local Similarity 53.8%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14  
:|||||  
Db 82 RRKEYDTLGHSAF 94

RESULT 39  
US-09-949-016-6832  
; Sequence 6832, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6832  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6832

Query Match 50.6%; Score 41; DB 4; Length 223;  
Best Local Similarity 53.8%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14  
:|||||  
Db 82 RRKEYDTLGHSAF 94

RESULT 40

US-09-949-016-11497  
; Sequence 11497, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11497  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11497

Query Match 50.6%; Score 41; DB 4; Length 267;  
Best Local Similarity 53.8%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAF 14  
:|||||  
Db 126 RRKEYDTLGHSAF 138

RESULT 41  
US-08-974-546-1  
; Sequence 1, Application US/08974546  
; Patent No. 5945287  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,546  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0428  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRAITUT21  
; CLONE: 2525691  
US-08-974-546-1

Query Match 50.6%; Score 41; DB 2; Length 348;  
Best Local Similarity 70.0%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYQ 10  
Db 59 KKRGLYDQYQ 68

## RESULT 42

US-09-543-681A-7130  
; Sequence 7130, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543.681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7130  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis

US-09-543-681A-7130

Query Match 50.6%; Score 41; DB 4; Length 387;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14  
Db 356 QKTAAYGHFGRAEF 369

## RESULT 43

US-09-252-991A-29230  
; Sequence 29230, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29230  
; LENGTH: 845  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29230

Query Match 50.6%; Score 41; DB 4; Length 845;  
Best Local Similarity 61.5%; Pred. No. 52;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RAAAYDQYGHAAFE 15

Db 408 RSAADQLGHGALE 420

## RESULT 44

US-09-902-540-14837  
; Sequence 14837, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkie, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 14837  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus

US-09-902-540-14837

Query Match 49.4%; Score 40; DB 4; Length 231;  
Best Local Similarity 60.0%; Pred. No. 20;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGH 11  
Db 201 ERAAYEHFGH 210

## RESULT 45

US-09-328-352-8169  
; Sequence 8169, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 8169  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii

US-09-328-352-8169

Query Match 49.4%; Score 40; DB 4; Length 317;  
Best Local Similarity 46.7%; Pred. No. 28;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 217 EKKAALDKLAHFAFK 231

## RESULT 46

US-09-252-991A-18102  
; Sequence 18102, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18

```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18102
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18102

Query Match      49.4%; Score 40; DB 4; Length 677;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      4 AAYDQYGHAAFE 15
Db      656 AAWDAYAHAAID 667

RESULT 47
US-09-252-991A-24992
; Sequence 24992, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24992
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24992

Query Match      49.4%; Score 40; DB 4; Length 915;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 RAAYDQYGHAAF 14
Db      614 RAAGERGHAAF 625

RESULT 48
US-09-248-796A-21361
; Sequence 21361, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21361
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21361
```

```
Query Match      48.1%; Score 39; DB 4; Length 116;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYQ 10
Db      96 QKYSAYDQWG 105

RESULT 49
US-08-619-554-4
; Sequence 4, Application US/08619554
; Patent No. 5821353
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS, Cameron M.
; APPLICANT: CHREBET, Gary L.
; APPLICANT: CLEMAS, Joseph
; APPLICANT: EL-SHERBEINI, Mohammed
; APPLICANT: FOOR, Forrest
; APPLICANT: KAHN, Jennifer,
; APPLICANT: KELLY, Rosemarie, - PARENT, S.A.
; APPLICANT: MARRINAN, Jean, - RAMADAN, N.M.
; APPLICANT: MORIN, Nancy, - REGISTER, E.A.
; APPLICANT: ONISHI, Janet, - SHEI, Gan-Ju
; TITLE OF INVENTION: DNA ENCODING 1,3 BETA-D GLUCAN
; TITLE OF INVENTION: SYNTHASE SUBUNITS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.
; STREET: 136 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,554
; FILING DATE: 01-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: COPPOLA, JOSEPH A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19104PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1895 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-619-554-4

Query Match      48.1%; Score 39; DB 2; Length 1895;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 QKRAAYDQYGHAAF 14
Db      31 QDQSAAYDEYGOPIY 44

RESULT 50
```

US-08-326-117B-3  
; Sequence 3, Application US/08326117B  
; Patent No. 5693491  
; GENERAL INFORMATION:  
; APPLICANT: BULLA, LEE A.  
; APPLICANT: JI, TAE  
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS  
; TITLE OF INVENTION: TOXIN  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/326,117B  
; FILING DATE: 19-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 7112-0037.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-326-117B-3

Query Match 46.9%; Score 38; DB 1; Length 107;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 70 EKIVKELYGHAVSE 84

RESULT 51  
US-08-982-129-3  
; Sequence 3, Application US/08982129  
; Patent No. 6007981  
; GENERAL INFORMATION:  
; APPLICANT: BULLA, LEE A.  
; APPLICANT: JI, TAE  
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS  
; TITLE OF INVENTION: TOXIN  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/982,129  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/326,117  
; APPLICATION NUMBER: US 08/326,117  
; FILING DATE: 19-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 7112-0037.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-982-129-3

Query Match 46.9%; Score 38; DB 3; Length 107;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 70 EKIVKELYGHAVSE 84

RESULT 52  
US-08-893-534A-5  
; Sequence 5, Application US/08893534A  
; Patent No. 6031072  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,534A  
; FILING DATE: 11-JUL-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-893-534A-5

Query Match 46.9%; Score 38; DB 3; Length 108;

```
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 53
US-08-996-679-5
; Sequence 5, Application US/08996679
; Patent No. 6169071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,853A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 32,391
; REFERENCE/DOCKET NUMBER: 100086.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-939-853A-7

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 54
US-08-939-853A-7
; Sequence 7, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 55
US-09-115-395-5
; Sequence 5, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115,395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-115-395-5

Query Match 46.9%; Score 38; DB 3; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 56
US-09-113-977C-38
; Sequence 38, Application US/09113977C
; Patent No. 6277824
```



; GENERAL INFORMATION:  
; APPLICANT: Doherty, Patrick  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE  
; FILE REFERENCE: 100086.403  
; CURRENT APPLICATION NUMBER: US/09/113.977C  
; CURRENT FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-113-977C-38

Query Match 46.9%; Score 38; DB 3; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 57  
US-09-507-102-5  
; Sequence 5, Application US/09507102  
; Patent No. 6326352  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED IP LAW GROUP PLLC  
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/507,102  
; FILING DATE: 17-Feb-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/893,534  
; FILING DATE: 11-JUL-1997  
; APPLICATION NUMBER: US 60/021,612  
; FILING DATE: 12-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Christensen, William T.  
; REGISTRATION NUMBER: 44,614  
; REFERENCE/DOCKET NUMBER: 100086.401C10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-507-102-5

Query Match 46.9%; Score 38; DB 3; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 58  
US-09-250-059-5  
; Sequence 5, Application US/09250059  
; Patent No. 6333307  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C6  
; CURRENT APPLICATION NUMBER: US/09/250,059  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-250-059-5

Query Match 46.9%; Score 38; DB 3; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 59  
US-09-248-074-5  
; Sequence 5, Application US/09248074  
; Patent No. 6346512  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C5  
; CURRENT APPLICATION NUMBER: US/09/248,074  
; CURRENT FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-248-074-5

Query Match 46.9%; Score 38; DB 3; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 60  
US-09-357-717-5  
; Sequence 5, Application US/09357717  
; Patent No. 6417325  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz

```

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
; FILE REFERENCE: 100086.401C7
; CURRENT APPLICATION NUMBER: US/09/357,717
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-357-717-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 61
US-09-458-870-5
; Sequence 5, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-458-870-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 62
US-09-351-048A-38
; Sequence 38, Application US/09351048A
; Patent No. 6472368
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; FILE REFERENCE: 100086.403C1
; CURRENT APPLICATION NUMBER: US/09/351,048A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

US-09-351-048A-38
; Sequence 38, Application US/09351048A
; Patent No. 6472368
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-544-782-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 63
US-09-248-015-5
; Sequence 5, Application US/09248015
; Patent No. 6562786
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 100086.401C4
; CURRENT APPLICATION NUMBER: US/09/248,015
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-248-015-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 64
US-09-544-782-5
; Sequence 5, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-544-782-5

Query Match 46.9%; Score 38; DB 4; Length 108;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15
Db 69 EKIVKELYGHAVSE 83

RESULT 65
US-10-058-821-5
; Sequence 5, Application US/10058821
; Patent No. 6780845
```

GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farooqui, Rizq  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY  
; FILE REFERENCE: 100086.401C12  
; CURRENT APPLICATION NUMBER: US/10/058,821  
; CURRENT FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-058-821-5

Query Match 46.9%; Score 38; DB 4; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 66  
US-10-193-653-38  
; Sequence 38, Application US/10193653  
; Patent No. 6806255  
; GENERAL INFORMATION:  
; APPLICANT: Doherty, Patrick  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE  
; TITLE OF INVENTION: FUNCTION  
; FILE REFERENCE: 100086.403C2  
; CURRENT APPLICATION NUMBER: US/10/193,653  
; CURRENT FILING DATE: 2002-07-10  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-10-193-653-38

Query Match 46.9%; Score 38; DB 4; Length 108;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 69 EKIVKELYGHAVSE 83

RESULT 67  
US-09-178-176B-8  
; Sequence 8, Application US/09178176B  
; Patent No. 6423502  
; GENERAL INFORMATION:  
; APPLICANT: BULLA, Lee A.  
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS  
; TITLE OF INVENTION: TOXIN  
; FILE REFERENCE: 27112-20037.11  
; CURRENT APPLICATION NUMBER: US/09/178,176B  
; CURRENT FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: US 08/982,129  
; PRIOR FILING DATE: 1997-12-01  
; PRIOR APPLICATION NUMBER: US 08/326,117  
; PRIOR FILING DATE: 1994-10-19

NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: M. sexta  
US-09-178-176B-8

Query Match 46.9%; Score 38; DB 4; Length 109;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 70 EKIVKELYGHAVSE 84

RESULT 68  
US-09-457-864-8  
; Sequence 8, Application US/09457864  
; Patent No. 6455266  
; GENERAL INFORMATION:  
; APPLICANT: Pioneer HiBred International  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS  
; TITLE OF INVENTION: TOXIN  
; FILE REFERENCE: 27112-20037.13  
; CURRENT APPLICATION NUMBER: US/09/457,864  
; CURRENT FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 08/326,117  
; PRIOR FILING DATE: 1994-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-457-864-8

Query Match 46.9%; Score 38; DB 4; Length 109;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 70 EKIVKELYGHAVSE 84

RESULT 69  
US-09-457-865A-8  
; Sequence 8, Application US/09457865A  
; Patent No. 6613886  
; GENERAL INFORMATION:  
; APPLICANT: Pioneer HiBred International  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS  
; TITLE OF INVENTION: TOXIN  
; FILE REFERENCE: 27112-20037.14  
; CURRENT APPLICATION NUMBER: US/09/457,865A  
; CURRENT FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 09/178,176  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: US 08/982,129  
; PRIOR FILING DATE: 1997-12-01  
; PRIOR APPLICATION NUMBER: US 08/326,117  
; PRIOR FILING DATE: 1994-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-457-865A-8

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Query Match 46.9%; Score 38; DB 4; Length 109;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 70 EKIVKELYGHAVSE 84

RESULT 70
US-09-513-999C-5896
; Sequence 5896, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5896
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5896

Query Match 46.9%; Score 38; DB 4; Length 119;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 73 QTRAIYDIYKRGLE 87

RESULT 71
US-09-489-039A-7692
; Sequence 7692, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7692
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7692

Query Match 46.9%; Score 38; DB 4; Length 554;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RAAYDQYGHAAFE 15
Db 250 RLGYEYGAAGFQ 262

RESULT 72
US-08-474-067-9
; Sequence 9, Application US/08474067
; Patent No. 5811518
; GENERAL INFORMATION:
; APPLICANT: Ranscht, Barbara
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/474,067
; APPLICATION NUMBER: US 08/474,067
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,361
; FILING DATE: 14-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/607,293
; FILING DATE: 30-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1682
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-474-067-9

Query Match 46.9%; Score 38; DB 2; Length 822;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 168 EKIVKELYGHAVSE 182

RESULT 73
US-08-474-068A-9
; Sequence 9, Application US/08474068A
; Patent No. 5837525
; GENERAL INFORMATION:
; APPLICANT: Ranscht, Barbara
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,068A
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/ FILING DATE: 07-JUN-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/213,361  
/ FILING DATE: 14-MAY-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/607,293  
/ FILING DATE: 30-OCT-1990  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Campbell, Cathryn A.  
/ REGISTRATION NUMBER: 31,815  
/ REFERENCE/DOCKET NUMBER: P-LJ 1686  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (619) 535-9001  
/ TELEFAX: (619) 535-8949  
/ INFORMATION FOR SEQ ID NO: 9:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 822 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
US-08-474-068A-9.

Query Match 46.9%; Score 38; DB 2; Length 822;  
Best Local Similarity 46.7%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGHAAFE 15  
:|:|||||  
Db 168 EKIVKELYGHAVSE 182

RESULT 74  
US-08-472-481-8  
; Sequence 8, Application US/08472481  
; Patent No. 5863804  
; GENERAL INFORMATION:  
; APPLICANT: Ranscht, Barbara  
; TITLE OF INVENTION: T-Cadherin Adhesion Molecule  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,481  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/213,361  
; FILING DATE: 14-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/607,293  
; FILING DATE: 30-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1686  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 822 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-472-481-8

Query Match 46.9%; Score 38; DB 2; Length 822;  
Best Local Similarity 46.7%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGHAAFE 15  
:|:|||||  
Db 168 EKIVKELYGHAVSE 182

RESULT 75  
US-09-513-999C-6016  
; Sequence 6016, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6016  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6016

Query Match 45.7%; Score 37; DB 4; Length 75;  
Best Local Similarity 60.0%; Pred. No. 20;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYXG 10  
:|:|||||  
Db 61 EKRELYDRYG 70

RESULT 76  
US-09-134-000C-5008  
; Sequence 5008, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5008  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-5008

Query Match 45.7%; Score 37; DB 4; Length 242;  
Best Local Similarity 63.6%; Pred. No. 71;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AYDOYGHAAFE 15  
:|:|||||  
Db 82 AYDOYALKAFQ 92

```
RESULT 77
US-09-248-796A-17629
; Sequence 17629, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17629
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (313),(314),(316),(318),(319)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-17629

Query Match 45.7%; Score 37; DB 4; Length 320;
Best Local Similarity 40.0%; Pred. No. 95;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 67 KQDIYDKYGEAGID 81

RESULT 78
US-09-198-452A-48
; Sequence 48, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 48
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-48

Query Match 45.7%; Score 37; DB 4; Length 392;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10
DB 58 QKRDSDYDRFG 67

RESULT 79
US-09-438-185A-34
; Sequence 34, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
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; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0032
US-09-438-185A-34

Query Match 45.7%; Score 37; DB 4; Length 406;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10
DB 72 QKRDSDYDRFG 81

RESULT 80
US-09-134-000C-5523
; Sequence 5523, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5523
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5523

Query Match 45.7%; Score 37; DB 4; Length 434;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
DB 230 KQAOYQQQGVIAFE 243

RESULT 81
US-09-489-039A-10301
; Sequence 10301, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10301
; LENGTH: 556
```

; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10301

Query Match 45.7%; Score 37; DB 4; Length 556;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAYDQYGH 11  
|:|:|:|:|  
Db 149 ASYFQYGH 156

RESULT 82  
US-09-244-805-27

; Sequence 27, Application US/09244805  
; Patent No. 6699660  
; GENERAL INFORMATION:  
; APPLICANT: Worley, Paul F.  
; APPLICANT: Lanahan, Anthony  
; APPLICANT: Goetz, Bernard  
; APPLICANT: Heimisch, Holger  
; APPLICANT: Kuner, Rohini  
; APPLICANT: Scheek, Sigrid  
; APPLICANT: Nikolich, Karoly  
; APPLICANT: Zhukovski, Eugene  
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 10496/004001  
; CURRENT APPLICATION NUMBER: US/09/244,805  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/074,518  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: 60/074,135  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 581  
; TYPE: PRT  
; ORGANISM: Eukaryote  
US-09-244-805-27

Query Match 45.7%; Score 37; DB 4; Length 581;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
|:|:|:|:|:|  
Db 71 KRAPERPGHVAFD 84

RESULT 83

US-09-252-991A-27230  
; Sequence 27230, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27230  
; LENGTH: 953  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27230

Query Match 45.7%; Score 37; DB 4; Length 953;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12  
|:|:|:|:|:|  
Db 518 RQRGAEEQFGHA 529

RESULT 84

US-08-346-849-8  
; Sequence 8, Application US/08346849  
; Patent No. 5670483  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Shuguang  
; APPLICANT: Lockshin, Curtis  
; APPLICANT: Rich, Alexander  
; APPLICANT: Holmes, Todd  
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
; TITLE OF INVENTION: THEREFOR  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/346,849  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/973,326  
; FILING DATE: 28 DECEMBER 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: MIT-6008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-346-849-8

Query Match 44.4%; Score 36; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYD 7  
|:|:|:|:|  
Db 46 QKRAAYD 52

RESULT 85

US-08-293-284A-8  
; Sequence 8, Application US/08293284A  
; Patent No. 5955343  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd  
; APPLICANT: Zhang, Shuguang

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;
; APPLICANT: Rich, Alexander
; APPLICANT: Dipersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-293-284A-8

Query Match 44.4%; Score 36; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7
Db 46 QKRAAYD 52

RESULT 86
US-08-898-300-8
; Sequence 8, Application US/08898300
; Patent No. 6548630
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,284
; FILING DATE: August 22, 1998
; PRIOR APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/898,300
; FILING DATE: 22 JULY 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,849
; FILING DATE: 30 NOVEMBER 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008FB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-898-300-8

Query Match 44.4%; Score 36; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7
Db 46 QKRAAYD 52

RESULT 87
US-08-824-513-8
; Sequence 8, Application US/08824513
; Patent No. 6800481
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: Dipersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/824,513
; FILING DATE: March 26, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,284
; FILING DATE: August 22, 1998
; PRIOR APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
```



NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 861-6240  
TELEFAX: (781) 861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-824-513-8

Query Match 44.4%; Score 36; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYD 7  
Db 46 QKRAAYD 52

RESULT 88  
US-09-513-999C-5565  
; Sequence 5565, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5565  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-5565

Query Match 44.4%; Score 36; DB 4; Length 65;  
Best Local Similarity 63.6%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAYDQYGHAAF 14  
Db 54 AAYDRNGNQAF 64

RESULT 89  
US-09-270-767-47445  
; Sequence 47445, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47445  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-47445

Query Match 44.4%; Score 36; DB 4; Length 130;  
Best Local Similarity 46.7%; Pred. No. 55;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 15  
Db 1 EKDLAYEAGGNAAFQ 15

RESULT 90  
US-09-513-999C-6925  
; Sequence 6925, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6925  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6925

Query Match 44.4%; Score 36; DB 4; Length 147;  
Best Local Similarity 66.7%; Pred. No. 63;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYG 10  
Db 138 KRLRYDEYG 146

RESULT 91  
US-09-270-767-46278  
; Sequence 46278, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46278  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-46278

Query Match 44.4%; Score 36; DB 4; Length 152;  
Best Local Similarity 66.7%; Pred. No. 65;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYG 10  
Db 16 KREVDYKYG 24

RESULT 92  
US-09-621-976-5129  
; Sequence 5129, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5129  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-621-976-5129

Query Match 44.4%; Score 36; DB 4; Length 153;  
Best Local Similarity 60.0%; Pred. No. 66;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 10  
Db 60 EKRDYDKYG 69

RESULT 93  
US-09-270-767-32870  
; Sequence 32870, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32870  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-32870

Query Match 44.4%; Score 36; DB 4; Length 175;  
Best Local Similarity 61.5%; Pred. No. 76;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAA 13  
Db 17 QNQAQDQYGTAA 29

RESULT 94  
US-09-270-767-48087  
; Sequence 48087, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48087  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-48087

Query Match 44.4%; Score 36; DB 4; Length 175;  
Best Local Similarity 61.5%; Pred. No. 76;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAA 13  
Db 17 QNQAQDQYGTAA 29

RESULT 95  
US-09-543-681A-7507  
; Sequence 7507, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7507  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7507

Query Match 44.4%; Score 36; DB 4; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DQYGHAA 12  
Db 184 DQYGHAA 189

RESULT 96  
US-09-248-796A-19977  
; Sequence 19977, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19977  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19977

Query Match 44.4%; Score 36; DB 4; Length 330;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 10  
Db 25 EKRRYDQFG 34

RESULT 97  
US-09-665-479A-8  
; Sequence 8, Application US/09665479A  
; Patent No. 6673570  
; GENERAL INFORMATION:  
; APPLICANT: Itoh, Fumiko  
; APPLICANT: Itoh, Susumu  
; APPLICANT: Heidin, Carl-Henrik

; APPLICANT: ten-Dijke, Peter  
; TITLE OF INVENTION: SWAD ASSOCIATING POLYPEPTIDES  
; FILE REFERENCE: L00461.70096.US  
; CURRENT APPLICATION NUMBER: US/09/665.479A  
; CURRENT FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US 60/154,846  
; PRIOR FILING DATE: 1999-09-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-665-479A-8

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Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 59 KKEIYDQFG 68

RESULT 98  
US-09-489-039A-10623  
; Sequence 10623, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 10623  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10623

Query Match 44.4%; Score 36; DB 4; Length 387;  
Best Local Similarity 53.8%; Pred. No. 1.8e+02;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db 266 KRYAFDPQKHAAY 278

RESULT 99  
US-09-252-991A-26237  
; Sequence 26237, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26237  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26237

Query Match 44.4%; Score 36; DB 4; Length 412;  
Best Local Similarity 46.7%; Pred. No. 1.9e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Db 29 QRRVAHQAGQAVLE 43

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US-09-252-991A-21980  
; Sequence 21980, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21980  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21980

Query Match 44.4%; Score 36; DB 4; Length 487;  
Best Local Similarity 72.7%; Pred. No. 2.2e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:55:33 ; Search time 165 Seconds

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Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	81	100.0	15	14	US-10-001-938-27
4	81	100.0	15	14	US-10-299-540-4
5	81	100.0	15	14	US-10-299-184-4
6	81	100.0	15	14	US-10-239-313A-444
7	81	100.0	15	16	US-10-614-639A-10
8	81	100.0	15	17	US-10-614-414A-10
9	81	100.0	16	14	US-10-001-938-3
10	81	100.0	16	14	US-10-239-313A-447
11	81	100.0	340	9	US-09-764-868-1153
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					Sequence 10, Appl
					Sequence 27, Appl
					Sequence 4, Appl
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					Sequence 444, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 3, Appl
					Sequence 447, Appl
					Sequence 1153, Ap

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378	100.0	15	US-10-369-493-386	Sequence 386, App
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72	88.9	15	US-10-299-184-5	Sequence 5, Appl
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84	45	15	US-09-833-245-653	Sequence 653, App

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89 44 54.3 168 16 US-10-767-701-57856 Sequence 57856, A
90 44 54.3 173 16 US-10-425-115-197095 Sequence 197095,
91 44 54.3 183 16 US-10-425-115-295514 Sequence 295514,
92 44 54.3 192 16 US-10-425-115-295500 Sequence 295500,
93 44 54.3 194 16 US-10-425-115-295516 Sequence 295516,
94 44 54.3 211 16 US-10-767-701-47401 Sequence 47401, A
95 44 54.3 212 16 US-10-425-115-309309 Sequence 309309,
96 44 54.3 217 15 US-10-424-599-271036 Sequence 271036,
97 44 54.3 244 16 US-10-425-115-217751 Sequence 217751,
98 44 54.3 273 16 US-10-437-963-157461 Sequence 157461,
99 44 54.3 352 14 US-10-077-584-8 Sequence 8, Appli
100 44 54.3 363 16 US-10-425-115-304214 Sequence 304214,
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## ALIGNMENTS

## RESULT 1

US-09-756-983-10

; Sequence 10, Application US/09756983

; Patent No. US20020122818A1

; GENERAL INFORMATION:

; APPLICANT: Albani, Salvatore

; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,

; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF

; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS

; FILE REFERENCE: 246/285-CIP

; CURRENT APPLICATION NUMBER: US/09/756,983

; CURRENT FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: 60/105,018

; PRIOR FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 09/421,506

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: PCT/US99/2466

; PRIOR FILING DATE: 1999-10-19

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 15

; TYPE: PRT

; ORGANISM: E. coli

; FEATURE:

; OTHER INFORMATION: dnaJpl heat shock protein

US-09-756-983-10

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Query Match 100.0%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

## RESULT 2

US-09-828-574-10

; Sequence 10, Application US/09828574

; Patent No. US20020146759A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: ALBANI, Salvatore

; APPLICANT: PRACKEN, Berent J.

; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF

; FILE REFERENCE: UCSD1310-1

; CURRENT APPLICATION NUMBER: US/09/828,574

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/224,104

; PRIOR FILING DATE: 2000-08-09

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: dnaJpl peptide

US-09-828-574-10

Query Match 100.0%; Score 81; DB 9; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 1 QKRAAYDQYGHAAFE 15

## RESULT 3

US-10-001-938-27

; Sequence 27, Application US/10001938

; Publication No. US20030031679A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: ALBANI, Salvatore

; APPLICANT: CARSON, Dennis

; APPLICANT: MARTINI, Alberto

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: UCSD1360-1

; CURRENT APPLICATION NUMBER: US/10/001,938

; CURRENT FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: US 60/245,181

; PRIOR FILING DATE: 2000-11-01

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 27

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-001-938-27

Query Match 100.0%; Score 81; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QKRAAYDQYGHAAFE 15

## RESULT 4

US-10-299-540-4

; Sequence 4, Application US/10299540

; Publication No. US20030143238A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: CARSON, Dennis A.

; APPLICANT: ALBANI, Salvatore

; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC

; TITLE OF INVENTION: AGAINST ARTHRITIS

; FILE REFERENCE: UCSD1370-7

; CURRENT APPLICATION NUMBER: US/10/299,540

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: US 09/616,247

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/107,615

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 08/618,464

; PRIOR FILING DATE: 1996-03-15

; PRIOR APPLICATION NUMBER: US 08/246,988

; PRIOR FILING DATE: 1994-05-20  
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; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic dnaJp1  
US-10-299-540-4

Query Match 100.0%; Score 81; DB 14; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15  
Db 1 OKRAAYDOYGHAAFE 15

## RESULT 5

US-10-299-184-4  
; Sequence 4, Application US/10299184  
; Publication No. US20030147910A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: CARSON, Dennis A.  
; APPLICANT: ALBANI, Salvatore

; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION  
; TITLE OF INVENTION: AGAINST ARTHRITIS  
; FILE REFERENCE: UCSD1370-6  
; CURRENT APPLICATION NUMBER: US/10/299,184  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: US 09/616,247  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/107,615  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 08/618,464  
; PRIOR FILING DATE: 1996-03-15  
; PRIOR APPLICATION NUMBER: US 08/246,988  
; PRIOR FILING DATE: 1994-05-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic dnaJp1  
US-10-299-184-4

Query Match 100.0%; Score 81; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15  
Db 1 OKRAAYDOYGHAAFE 15

## RESULT 6

US-10-239-313A-444  
; Sequence 444, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGNER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane

; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 444  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-444

Query Match 100.0%; Score 81; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15  
Db 1 OKRAAYDOYGHAAFE 15

## RESULT 7

US-10-614-639A-10  
; Sequence 10, Application US/10614639A  
; Publication No. US20040224009A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBANI, Salvatore  
; TITLE OF INVENTION: METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION  
; TITLE OF INVENTION: AND MODULATION OF ANTIGEN-SPECIFIC T CELLS  
; FILE REFERENCE: AND-TCCIP1-DIV2  
; CURRENT APPLICATION NUMBER: US/10/614,639A  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: 09/756,983  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: PCT/US99/24666  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 09/421,506  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/105,018  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-614-639A-10

Query Match 100.0%; Score 81; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFE 15  
Db 1 OKRAAYDOYGHAAFE 15

## RESULT 8

US-10-614-414A-10  
; Sequence 10, Application US/10614414A  
; Publication No. US20050079208A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBANI, Salvatore  
; TITLE OF INVENTION: METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION  
; TITLE OF INVENTION: AND MODULATION OF ANTIGEN-SPECIFIC T CELLS  
; FILE REFERENCE: AND-TCCIP1-DIV1  
; CURRENT APPLICATION NUMBER: US/10/614,414A  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: 09/756,983  
; PRIOR FILING DATE: 2001-01-09

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; PRIOR APPLICATION NUMBER: PCT/US99/24666
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-614-414A-10

Query Match          100.0%; Score 81; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match          100.0%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 10
US-10-239-313A-447
; Sequence 447, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711

; PRIOR APPLICATION NUMBER: PCT/US99/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-447

Query Match          100.0%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
US-09-764-868-1153
; Sequence 1153, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (196)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1153

Query Match          100.0%; Score 81; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 25 QKRAAYDQYGHAAFE 39

RESULT 12
US-09-764-868-1152
; Sequence 1152, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```



; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1152  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-868-1152

Query Match 100.0%; Score 81; DB 9; Length 341;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 26 QKRAAYDQYGHAAFE 40  
|||||

## RESULT 13

US-10-369-493-689

; Sequence 689, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 689

; LENGTH: 376

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-369-493-689

Query Match 100.0%; Score 81; DB 15; Length 376;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 61 QKRAAYDQYGHAAFE 75  
|||||

## RESULT 14

US-10-369-493-386

; Sequence 386, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 386  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Xenorhabdus nematophilus  
US-10-369-493-386

Query Match 100.0%; Score 81; DB 15; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 61 QKRAAYDQYGHAAFE 75  
|||||

## RESULT 15

US-10-369-493-21305

; Sequence 21305, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21305

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Xenorhabdus nematophilus

US-10-369-493-21305

Query Match 100.0%; Score 81; DB 15; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 61 QKRAAYDQYGHAAFE 75  
|||||

## RESULT 16

US-10-369-493-10648

; Sequence 10648, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 10648

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Sphingomonas aromaticivorans

US-10-369-493-10648

Query Match 91.4%; Score 74; DB 15; Length 365;

Best Local Similarity 86.7%; Pred. No. 0.00023; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
DB 56 OKRAAYDRYGHAAQF 70

RESULT 17  
US-10-369-493-12087  
; Sequence 12087, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 12087  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Mesorhizobium loti  
US-10-369-493-12087

Query Match 90.1%; Score 73; DB 15; Length 376;  
Best Local Similarity 86.7%; Pred. No. 0.00035; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
DB 60 OKRAAYDRYGHAAFE 74

RESULT 18  
US-09-828-574-11  
; Sequence 11, Application US/09828574  
; Patent No. US20020146759A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: ALBANI, Salvatore  
; APPLICANT: PRAKSEN, Berent J.  
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF  
; FILE REFERENCE: UCSD1310-1  
; CURRENT APPLICATION NUMBER: US/09/828,574  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/224,104  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Irrelevant dnaJpV peptide  
US-09-828-574-11

Query Match 88.9%; Score 72; DB 9; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.9e-05; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
DB 2 ERAAYDQYGHAAFE 15

RESULT 19  
US-10-299-540-5  
; Sequence 5, Application US/10299540  
; Publication No. US20030143238A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: CARSON, Dennis A.  
; APPLICANT: ALBANI, Salvatore  
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC  
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF R  
; TITLE OF INVENTION: ARTHRITIS  
; FILE REFERENCE: UCSD1370-7  
; CURRENT APPLICATION NUMBER: US/10/299,540  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US 09/616,247  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/107,615  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 08/618,464  
; PRIOR FILING DATE: 1996-03-15  
; PRIOR APPLICATION NUMBER: US 08/246,988  
; PRIOR FILING DATE: 1994-05-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Mutant dnaJ peptide  
US-10-299-540-5

Query Match 88.9%; Score 72; DB 14; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.9e-05; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
DB 2 ERAAYDQYGHAAFE 15

RESULT 20  
US-10-299-184-5  
; Sequence 5, Application US/10299184  
; Publication No. US20030147910A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: CARSON, Dennis A.  
; APPLICANT: ALBANI, Salvatore  
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC  
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF R  
; TITLE OF INVENTION: ARTHRITIS  
; FILE REFERENCE: UCSD1370-6  
; CURRENT APPLICATION NUMBER: US/10/299,184  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US 09/616,247  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/107,615  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 08/618,464  
; PRIOR FILING DATE: 1996-03-15  
; PRIOR APPLICATION NUMBER: US 08/246,988  
; PRIOR FILING DATE: 1994-05-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Mutant dnaJ peptide  
US-10-299-184-5

Query Match 88.9%; Score 72; DB 14; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.9e-05;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||:|||||  
Db 2 ERAAYDQYGHAAFE 15

RESULT 21  
US-10-369-493-8065  
; Sequence 8065, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 8065  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Rhodobacter sphaeroides  
US-10-369-493-8065

Query Match 85.2%; Score 69; DB 15; Length 382;  
Best Local Similarity 85.7%; Pred. No. 0.0017;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||:|||||  
Db 62 KKAAYDRYGHAAFE 75

RESULT 22  
US-10-369-493-21849  
; Sequence 21849, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 21849  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Rhodobacter capsulatus  
US-10-369-493-21849

Query Match 85.2%; Score 69; DB 15; Length 384;  
Best Local Similarity 85.7%; Pred. No. 0.0018;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
:|||||:|||||

Db 62 KKAAYDRYGHAAFE 75

RESULT 23  
US-10-375-010-22  
; Sequence 22, Application US/10375010  
; Publication No. US20040170985A1  
; GENERAL INFORMATION:  
; APPLICANT: USUDA, Yoshihiro  
; APPLICANT: NISHIO, Yosuke  
; APPLICANT: YASUEDA, Hisashi  
; APPLICANT: SUGIMOTO, Shinichi  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN THE STRESS RES  
; FILE REFERENCE: 232744US0  
; CURRENT APPLICATION NUMBER: US/10/375,010  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Methylophilus methylotrophus  
US-10-375-010-22

Query Match 82.7%; Score 67; DB 16; Length 376;  
Best Local Similarity 80.0%; Pred. No. 0.0038;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|||||:|||||  
Db 63 QKRAAYDQYGHAGVD 77

RESULT 24  
US-10-369-493-7330  
; Sequence 7330, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 7330  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Burkholderia cepacia  
US-10-369-493-7330

Query Match 82.7%; Score 67; DB 15; Length 379;  
Best Local Similarity 80.0%; Pred. No. 0.0038;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|||||:|||||  
Db 61 QKRAAYDQYGHAGVD 75

RESULT 25  
US-10-369-493-4573  
; Sequence 4573, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei

```
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4573
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4573

Query Match      82.7%; Score 67; DB 15; Length 380;
Best Local Similarity 80.0%; Pred. No. 0.0038;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 OKRAAYDQYGHAGVD 75

RESULT 26
US-10-369-493-47
; Sequence 47, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 47
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-10-369-493-47

Query Match      77.8%; Score 63; DB 15; Length 376;
Best Local Similarity 73.3%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 63 EKRLYDMYGHAAFE 77

RESULT 27
US-10-369-493-13658
; Sequence 13658, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
```

```
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13658
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13658

Query Match      76.5%; Score 62; DB 15; Length 374;
Best Local Similarity 78.6%; Pred. No. 0.027;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 62 KRAAYDQYGHAGVD 75

RESULT 28
US-10-369-493-8450
; Sequence 8450, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8450
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-10-369-493-8450

Query Match      75.3%; Score 61; DB 15; Length 378;
Best Local Similarity 66.7%; Pred. No. 0.041;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 EKRAAYDQYGHAGVD 75

RESULT 29
US-10-369-493-15859
; Sequence 15859, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15859
; LENGTH: 375
```

; TYPE: PRT  
; ORGANISM: Xanthomonas campestris  
US-10-369-493-15859

Query Match 74.1%; Score 60; DB 15; Length 375;  
Best Local Similarity 78.6%; Pred. No. 0.061;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15  
Db 62 KRAYDAHGHAFFE 75

## RESULT 30

US-10-369-493-15487  
; Sequence 15487, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 15487

; LENGTH: 376  
; TYPE: PRT

; ORGANISM: Xanthomonas campestris  
US-10-369-493-15487

Query Match 74.1%; Score 60; DB 15; Length 376;  
Best Local Similarity 78.6%; Pred. No. 0.061;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15  
Db 62 KRAYDAHGHAFFE 75

## RESULT 31

US-10-369-493-9641  
; Sequence 9641, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 9641

; LENGTH: 358  
; TYPE: PRT

; ORGANISM: Desulfitobacterium hafnense  
US-10-369-493-9641

Query Match 72.8%; Score 59; DB 15; Length 358;  
Best Local Similarity 66.7%; Pred. No. 0.086;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 46 EKRAYDQMGHSAFD 60

## RESULT 32

US-10-369-493-18523  
; Sequence 18523, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 18523

; LENGTH: 379  
; TYPE: PRT

; ORGANISM: Lactococcus lactis  
US-10-369-493-18523

Query Match 71.6%; Score 58; DB 15; Length 379;  
Best Local Similarity 71.7%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHGA 12  
Db 60 QKRAAYDQYGEA 71

## RESULT 33

US-10-369-493-16754  
; Sequence 16754, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 16754

; LENGTH: 385  
; TYPE: PRT

; ORGANISM: Caulobacter crescentus  
US-10-369-493-16754

Query Match 71.6%; Score 58; DB 15; Length 385;  
Best Local Similarity 83.3%; Pred. No. 0.14;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHGA 12  
Db 59 QKRAAYDQYGEA 70

## RESULT 34

```

; FILE REFERENCE: AM100649-PCT
; CURRENT APPLICATION NUMBER: US/10/474,776
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 634
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-10-474-776--634

Query Match          69.1%; Score 56; DB 16; Length 378;
Best Local Similarity 91.7%; Pred.No. 0.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYCHA 12
Db 60 QKRAAYDQYGAA 71

RESULT 37
US-10-472-928-900
; Sequence 900, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 900
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: dnaJ protein (dnaJ)
; OTHER INFORMATION: Cellular location: cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15902500 (O.E+01)
; US-10-472-928-900

Query Match          69.1%; Score 56; DB 17; Length 378;
Best Local Similarity 91.7%; Pred.No. 0.3;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYCHA 12
Db 60 QKRAAYDQYGAA 71

RESULT 38
US-10-617-320-3487
; Sequence 3487, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660

```



; OTHER INFORMATION: Bacterial dnaJp2 peptide  
US-10-299-184-6

Query Match 66.7%; Score 54; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
Db 6 QKRAAYDQYG 15

## RESULT 42

US-10-425-115-239397  
; Sequence 239397, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; PRIOR FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 239397  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MPT4577\_149916C.1.pcp  
US-10-425-115-239397

Query Match 66.7%; Score 54; DB 16; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
Db 43 QKRAAYDQYG 52

## RESULT 43

US-10-369-493-10371  
; Sequence 10371, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 10371  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Cytophaga hutchinsonii  
US-10-369-493-10371

Query Match 64.2%; Score 52; DB 15; Length 360;  
Best Local Similarity 69.2%; Pred. No. 1.4;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAA 13

Db 59 EKRRYDQYGHQA 71

## RESULT 44

US-10-369-493-23206  
; Sequence 23206, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 23206  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-10-369-493-23206

Query Match 64.2%; Score 52; DB 15; Length 372;  
Best Local Similarity 81.8%; Pred. No. 1.4;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
Db 60 QKRAHYDQFGH 70

## RESULT 45

US-10-369-493-1212  
; Sequence 1212, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 1212  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Methanobacterium thermoautotrophicum  
US-10-369-493-1212

Query Match 64.2%; Score 52; DB 15; Length 376;  
Best Local Similarity 53.3%; Pred. No. 1.4;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
Db 60 EKRAHYDQFGHAGMD 74

## RESULT 46

US-10-767-701-40315  
; Sequence 40315, Application US/10767701



Publication No. US20040172684A1  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
FILE REFERENCE: 38-21(53535)B  
CURRENT APPLICATION NUMBER: US/10/767,701  
CURRENT FILING DATE: 2004-01-29  
NUMBER OF SEQ ID NOS: 63128  
SEQ ID NO 40315  
LENGTH: 175  
TYPE: PRT  
ORGANISM: Sorghum bicolor  
FEATURE:  
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6829\_1.pep  
US-10-767-701-40315

Query Match 61.7%; Score 50; DB 16; Length 175;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
|||||  
Db 61 QGRAVYDQYG 70

## RESULT 47

US-10-425-115-289174  
Sequence 289174, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 289174  
LENGTH: 241  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_26817C.1.pep  
US-10-425-115-289174

Query Match 61.7%; Score 50; DB 16; Length 241;  
Best Local Similarity 90.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
|||||  
Db 61 QGRAVYDQYG 70

## RESULT 48

US-10-282-122A-54551  
Sequence 54551, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John

APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 54551  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Campylobacter jejuni  
US-10-282-122A-54551

Query Match 61.7%; Score 50; DB 15; Length 297;  
Best Local Similarity 64.3%; Pred. No. 2.5;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14  
:|||||  
Db 58 KKRAQYDQYGSWF 71

## RESULT 49

US-10-437-963-190831  
Sequence 190831, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 190831  
LENGTH: 362  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87208C.1.pep  
US-10-437-963-190831

```
Query Match      61.7%; Score 50; DB 16; Length 362;
Best Local Similarity 90.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
Db      61 QKRAVDQYG 70

RESULT 50
US-10-425-115-289176
; Sequence 289176, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289176
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26819C.1.pep
US-10-425-115-289176

Query Match      61.7%; Score 50; DB 16; Length 362;
Best Local Similarity 90.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
Db      61 QKRAVDQYG 70

RESULT 51
US-10-437-963-108162
; Sequence 108162, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108162
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_12442C.1.pep
US-10-437-963-108162

Query Match      61.7%; Score 50; DB 16; Length 383;
Best Local Similarity 90.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
```

```
Db      95 QKRAVDQYG 104

RESULT 52
US-10-425-114-59964
; Sequence 59964, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59964
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-244-F10_FLI.pep
US-10-425-114-59964

Query Match      61.7%; Score 50; DB 15; Length 404;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
Db      103 QKRAVDQYG 112

RESULT 53
US-10-424-599-191916
; Sequence 191916, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191916
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1531C.1.pep
US-10-424-599-191916

Query Match      60.5%; Score 49; DB 15; Length 146;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
Db      61 QKRAVDQYG 70

RESULT 54
US-10-425-115-206200
; Sequence 206200, Application US/10425115
```

Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 363326  
; SEQ ID NO 206200  
; LENGTH: 150  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(150)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_119639C.1.pep  
US-10-425-115-206200

Query Match 60.5%; Score 49; DB 16; Length 150;  
Best Local Similarity 75.0%; Pred. No. 1.9;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12  
Db 98 QKRAAYDQYGEA 109

## RESULT 55

US-10-425-114-48912  
; Sequence 48912, Application US/10425114  
; Publication No. US20040034889A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 48912  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3067-017-D1\_Flt.pep  
US-10-425-114-48912

Query Match 60.5%; Score 49; DB 15; Length 158;  
Best Local Similarity 90.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10  
Db 65 QKRAAYDQYGH 74

## RESULT 56

US-10-767-701-40388  
; Sequence 40388, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53353)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 40388  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C58008\_1.pep  
US-10-767-701-40388

Query Match 60.5%; Score 49; DB 16; Length 228;  
Best Local Similarity 75.0%; Pred. No. 2.9;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12  
Db 131 QKRAAYDQYGEA 142

## RESULT 57

US-10-424-599-144051  
; Sequence 144051, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 144051  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(311)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_101090C.1.pep  
US-10-424-599-144051

Query Match 60.5%; Score 49; DB 15; Length 311;  
Best Local Similarity 75.0%; Pred. No. 3.9;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12  
Db 120 QKRAAYDQYGEA 131

## RESULT 58

US-10-425-115-300448  
; Sequence 300448, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B

```
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 300448
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_37079C.1.pep
US-10-425-115-300448
```

```
Query Match          60.5%; Score 49; DB 16; Length 326;
Best Local Similarity 90.0%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 OKRAAYDQYG 10
         ||| ||| |||
Db      59 QKRAAYDQYG 68
```

```
RESULT 59
US-10-369-493-17209
; Sequence 17209, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17209
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17209
```

```
Query Match          60.5%; Score 49; DB 15; Length 370;
Best Local Similarity 72.7%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 OKRAAYDQYGH 11
         ||| ||| ||| |||
Db      60 QKRAHYDQFGH 70
```

```
RESULT 60
US-10-424-599-249417
; Sequence 249417, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 249417
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```

```
; NAME/KEY: unsure
; LOCATION: (1)...(485)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67253C.1.pep
US-10-424-599-249417
```

```
Query Match          60.5%; Score 49; DB 15; Length 485;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 OKRAAYDQYGH 12
         ||| ||| ||| |||
Db      123 KKRALYDQYGEA 134
```

```
RESULT 61
US-10-425-115-348539
; Sequence 348539, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 348539
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_81031C.1.pep
US-10-425-115-348539
```

```
Query Match          60.5%; Score 49; DB 16; Length 487;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 OKRAAYDQYGH 12
         ||| ||| ||| |||
Db      122 KKRALYDQYGEA 133
```

```
RESULT 62
US-10-437-963-123435
; Sequence 123435, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123435
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26270C.1.pep
```

## US-10-437-963-123435

Query Match 60.5%; Score 49; DB 16; Length 542;  
Best Local Similarity 75.0%; Pred. No. 6.9;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHHA 12  
Db 181 KKRALYDQYGEA 192

## RESULT 63

US-10-369-493-12619

; Sequence 12619, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 12619

; LENGTH: 423

; TYPE: PRT

; ORGANISM: Aspergillus nidulans

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(423)

; OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-12619

## Query Match

59.3%; Score 48; DB 15; Length 423;

Best Local Similarity

53.3%; Pred. No. 8;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15

Db 138 KKRETYDRFGSAAPD 152

## RESULT 64

US-10-369-493-21871

; Sequence 21871, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21871

; LENGTH: 511

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-21871

## Query Match

59.0%; Score 47; DB 15; Length 511;

## US-10-424-599-233524

; Sequence 233524, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 233524

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52899C.1.pap

US-10-424-599-233524

## Query Match

56.8%; Score 46; DB 15; Length 116;

Best Local Similarity

80.0%; Pred. No. 4.7;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10

Db 61 QKRAIYDEYG 70

## RESULT 66

US-10-425-115-295592

; Sequence 295592, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295592

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(135)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_32659C.1.pap

US-10-425-115-295592

## Query Match

56.8%; Score 46; DB 16; Length 135;

Best Local Similarity

60.0%; Pred. No. 5.5;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15

Db 117 KROQYDFGPAAF 129

```
Db      65 QKREYDQYGDALK 79
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7746
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C251922_1.p
US-10-739-930-7746
Query Match      56.8%; Score 46; DB 16; Length 352;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      :||| |||||
Db      73 EKRAIYDQYG 82

RESULT 70
US-10-739-930-7078
; Sequence 7078, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7078
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(382)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C508_15.p
US-10-739-930-7078
Query Match      56.8%; Score 46; DB 16; Length 382;
Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 QKRAAYDQYGHAAFE 15
      :||| |||||
Db      36 QRRATYGNYSNAAFQ 50

RESULT 71
US-10-424-599-3465
; Sequence 3465, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

Db      65 QKREYDQYGDALK 79
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 237535
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56519C.1.p
US-10-424-599-237535
Query Match      56.8%; Score 46; DB 15; Length 192;
Best Local Similarity 80.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      :||| |||||
Db      61 QKRGVYDQYG 70

RESULT 68
US-10-424-599-257471
; Sequence 257471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257471
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7451C.1.p
US-10-424-599-257471
Query Match      56.8%; Score 46; DB 15; Length 217;
Best Local Similarity 80.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QKRAAYDQYG 10
      :||| |||||
Db      61 QKRGVYDQYG 70

RESULT 69
US-10-739-930-7746
; Sequence 7746, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
```

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 3465  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
US-10-369-493-3465

Query Match 56.8%; Score 46; DB 15; Length 401;  
Best Local Similarity 53.3%; Pred. No. 17;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 68 EKRFQDFGGAAGFE 82

## RESULT 72

US-10-424-599-282287  
; Sequence 282287, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 282287  
; LENGTH: 427  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_96928C.1.pep  
US-10-424-599-282287

Query Match 56.8%; Score 46; DB 15; Length 427;  
Best Local Similarity 57.1%; Pred. No. 18;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAAF 14  
Db 145 EKRFQDFGVDGHAY 158

## RESULT 73

US-10-425-115-337892  
; Sequence 337892, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 337892  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(115)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_71325C.1.pep

## US-10-425-115-337892

Query Match 55.6%; Score 45; DB 16; Length 115;  
Best Local Similarity 80.0%; Pred. No. 6.9;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 10  
Db 62 QKRTIYDQYGH 71

## RESULT 74

US-10-425-114-72263  
; Sequence 72263, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53113)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 72263  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mexicana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE034C01\_FLI.pep  
US-10-425-114-72263

Query Match 55.6%; Score 45; DB 15; Length 133;  
Best Local Similarity 63.6%; Pred. No. 8;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 11  
Db 98 QQRVEYDQYGH 108

## RESULT 75

US-10-424-599-257493  
; Sequence 257493, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 257493  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_7453C.1.pep  
US-10-424-599-257493

Query Match 55.6%; Score 45; DB 15; Length 153;  
Best Local Similarity 80.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 10

```
Db 61 QKRGYDQYG 70
||| |||||
Query Match 55.6%; Score 45; DB 16; Length 340;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 76
US-09-833-245-652
; Sequence 652, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 652
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (204)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (305)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-652

Query Match 55.6%; Score 45; DB 11; Length 332;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12
: |||: |||||
Db 84 EKRSYDQYGD 95

RESULT 77
US-10-425-115-360745
; Sequence 360745, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 360745
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(340)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92181C.1.pep
US-10-425-115-360745

Db 63 KRAAYDQYG 71
||| |||||
Query Match 55.6%; Score 45; DB 16; Length 346;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 78
US-10-437-963-126854
; Sequence 126854, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126854
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29360C.1.pep
US-10-437-963-126854

Query Match 55.6%; Score 45; DB 16; Length 342;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
||| |||||
Db 62 QKRAAYDKYG 71

RESULT 79
US-10-739-930-6016
; Sequence 6016, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6016
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C207692_1.p
US-10-739-930-6016

Query Match 55.6%; Score 45; DB 16; Length 346;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10
||| |||||
Db 63 KRAAYDKYG 71
```



RESULT 80  
US-10-425-114-37469  
; Sequence 37469, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 37469  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-004-A3\_FLI.pep  
US-10-425-114-37469

Query Match 55.6%; Score 45; DB 15; Length 352;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10  
||| |||||  
DB 74 KRAVDQYG 82

RESULT 81  
US-10-437-963-126176  
; Sequence 126176, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 126176  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_28749C.1.pep  
US-10-437-963-126176

Query Match 55.6%; Score 45; DB 16; Length 356;  
Best Local Similarity 80.0%; Pred. No. 22;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
||| |||||  
DB 60 QKRAVDQFG 69

RESULT 82

US-10-104-047-2714  
; Sequence 2714, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2714  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2714

Query Match 55.6%; Score 45; DB 15; Length 595;  
Best Local Similarity 66.7%; Pred. No. 37;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGA 12  
: ||: |||||  
DB 84 EKRSNYDQYGA 95

RESULT 83  
US-10-322-281-574  
; Sequence 574, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 574  
; LENGTH: 696  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-322-281-574

Query Match 55.6%; Score 45; DB 16; Length 696;  
Best Local Similarity 66.7%; Pred. No. 44;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGA 12  
: ||: |||||  
DB 6 EKRSNYDQYGA 17

RESULT 84  
US-09-833-245-653  
; Sequence 653, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256,931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199,384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 653
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-653

Query Match      55.6%; Score 45; DB 11; Length 737;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHA 12
      :||: |||||
DB      84 EKRSNYDQYGDA 95

RESULT 85
US-10-756-149-5816
; Sequence 5816, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5816
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5816

Query Match      55.6%; Score 45; DB 18; Length 822;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHA 12
      :||: |||||
DB      124 EKRSNYDQYGDA 135

RESULT 86
US-10-425-115-337846
; Sequence 337846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337846
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71284C.1.pep
US-10-425-115-337846

Query Match      54.3%; Score 44; DB 16; Length 59;
Best Local Similarity 53.3%; Pred. No. 5.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHAAFE 15
      :||: |||||

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 653
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-653

Query Match      55.6%; Score 45; DB 11; Length 737;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHA 12
      :||: |||||
DB      84 EKRSNYDQYGDA 95

RESULT 87
US-10-425-115-341282
; Sequence 341282, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 341282
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_74415C.1.pep
US-10-425-115-341282

Query Match      54.3%; Score 44; DB 16; Length 94;
Best Local Similarity 61.5%; Pred. No. 8.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHAA 13
      :||: |||||
DB      54 EKRIYDQYGEDA 66

RESULT 88
US-10-425-115-205457
; Sequence 205457, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 205457
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(103)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_118964C.1.pep
US-10-425-115-205457

Query Match      54.3%; Score 44; DB 16; Length 103;
Best Local Similarity 53.3%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 OKRAAYDQYGHAAFE 15
      :||: |||||
```

Db 79 EKREIYDQYGEDALK 93

## RESULT 89

US-10-767-701-57856

; Sequence 57856, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 57856

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: 30973076.pep

US-10-767-701-57856

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 168;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 7 EKRSIYDKYGEAGLK 21

## RESULT 90

US-10-425-115-197095

; Sequence 197095, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 197095

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(173)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_111333C.1.pep

US-10-425-115-197095

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 173;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 131 EKRSIYDKYGEAGLK 145

## RESULT 91

US-10-425-115-295514

; Sequence 295514, Application -US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295514

; LENGTH: 183

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(183)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_32589C.1.pep

US-10-425-115-295514

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 183;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 65 EKREIYDQYGEDALK 79

## RESULT 92

US-10-425-115-295500

; Sequence 295500, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 295500

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(192)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_32576C.1.pep

US-10-425-115-295500

Query Match

Best Local Similarity 54.3%; Score 44; DB 16; Length 192;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

:||:|||||:

Db 65 EKREIYDQYGEDALK 79

## RESULT 93

US-10-425-115-295516

; Sequence 295516, Application US/10425115

; Publication No. US20040214272A1

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 295516
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(194)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_32590C.1.pep
US-10-425-115-295516

Query Match      54.3%; Score 44; DB 16; Length 194;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 OKRAAYDQYGHAAFE 15
Db      65 EKREIYDQYGEDALK 79

RESULT 94
US-10-767-701-47401
; Sequence 47401, Application US/107677701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47401
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(211)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3435_5.pep
US-10-767-701-47401

Query Match      54.3%; Score 44; DB 16; Length 211;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 OKRAAYDQYGHAAFE 15
Db      65 EKREIYDQYGEDALK 79

RESULT 95
US-10-425-115-309309
; Sequence 309309, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 309309
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(212)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_45155C.1.pep
US-10-425-115-309309

Query Match      54.3%; Score 44; DB 16; Length 212;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 OKRAAYDQYGHAAFE 15
Db      66 EKREIYDQYGEDALK 80

RESULT 96
US-10-424-599-271036
; Sequence 271036, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 271036
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_86764C.1.pep
US-10-424-599-271036

Query Match      54.3%; Score 44; DB 15; Length 217;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 OKRAAYDQYGHAAFE 15
Db      65 EKREIYDQYGEDALK 79

RESULT 97
US-10-425-115-217751
; Sequence 217751, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
```

; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 217751  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(244)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_130186C.1.pep  
US-10-425-115-217751

Query Match 54.3%; Score 44; DB 16; Length 244;  
Best Local Similarity 53.3%; Pred. No. 22;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 66 EKREIYDQYGEDAIK 80

## RESULT 98

US-10-437-963-157461  
; Sequence 157461, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 157461  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_5702C.1.pep  
US-10-437-963-157461

Query Match 54.3%; Score 44; DB 16; Length 273;  
Best Local Similarity 88.9%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQY 10  
Db 63 KRALYDQY 71

## RESULT 99

US-10-077-584-8  
; Sequence 8, Application US/10077584  
; Publication No. US20030073610A1  
; GENERAL INFORMATION:  
; APPLICANT: LINDQUIST, SUSAN  
; APPLICANT: KROBITSCH, SYLVIA  
; APPLICANT: OUTEIRO, TIAGO F.  
; TITLE OF INVENTION: YEAST SCREENS FOR THE TREATMENT OF HUMAN DISEASE  
; FILE REFERENCE: ARCD:367US  
; CURRENT APPLICATION NUMBER: US/10/077,584  
; CURRENT FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: 60/369,157  
; PRIOR FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-077-584-8

Query Match 54.3%; Score 44; DB 14; Length 352;  
Best Local Similarity 80.0%; Pred. No. 32;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQY 10  
Db 59 QKREIYDQY 68

## RESULT 100

US-10-425-115-304214  
; Sequence 304214, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 304214  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(363)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_40514C.1.pep  
US-10-425-115-304214

Query Match 54.3%; Score 44; DB 16; Length 363;  
Best Local Similarity 53.3%; Pred. No. 33;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
Db 66 EKREIYDQYGEDAIK 80

Search completed: September 2, 2005, 21:08:50  
Job time : 168 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:48:00 ; Search time 16 Seconds  
(without alignments)  
90.203 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81

Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	376	1	HHECDJ
2	81	100.0	376	2	G90630
3	81	100.0	376	2	G85481
4	81	100.0	379	2	AF0503
5	81	100.0	379	2	AB0058
6	81	100.0	394	2	C64112
7	78	96.3	381	2	D82270
8	77	95.1	392	2	S15295
9	75	92.6	377	2	F84947
10	75	92.6	377	2	JC5609
11	73	90.1	373	2	D81242
12	73	90.1	375	2	B47042
13	73	90.1	377	2	D97373
14	73	90.1	377	2	AD2591
15	73	90.1	377	2	AC3502
16	64	79.0	370	2	C71729
17	63	77.8	376	2	E70361
18	62	76.5	190	2	B35388
19	62	76.5	377	2	A83052
20	60	74.1	373	2	H97728
21	59	72.8	367	2	I40843
22	58	71.6	379	2	H86902
23	58	71.6	379	2	A47079
24	58	71.6	385	2	C87250
25	57	70.4	352	2	A49210
26	57	70.4	364	2	D70164
27	57	70.4	376	2	AD1621
28	57	70.4	377	2	T43739
29	57	70.4	377	2	AH1258

30	56	69.1	368	2	F82570	DnaJ protein XP233
31	56	69.1	372	2	H97928	heat-shock protein
32	56	69.1	378	2	D95060	dnaJ protein [impo
33	53	65.4	499	2	G96831	hypothetical prote
34	52	64.2	372	2	B41874	heat shock protein
35	52	64.2	376	2	H69038	heat shock protein
36	52	64.2	389	2	S41748	heat shock protein
37	50	61.7	297	2	G81329	probable curved-DN
38	50	61.7	348	2	T04618	heat shock protein
39	50	61.7	379	2	B89939	DnaJ protein [impo
40	50	61.7	383	2	E90603	heat shock protein
41	50	61.7	416	2	F71379	heat shock protein
42	49	60.5	370	2	D83818	heat-shock protein
43	49	60.5	375	2	D82894	heat shock protein
44	49	60.5	498	2	T06594	heat shock protein
45	48	59.3	380	2	JC4739	heat shock protein
46	48	59.3	385	1	S29852	ADP,ATP carrier pr
47	48	59.3	910	1	S73361	dnaJ homolog prote
48	47	58.0	337	2	G84590	probable heat shoc
49	47	58.0	511	2	S38898	heat shock protein
50	45	55.6	335	2	T48161	heat shock protein
51	45	55.6	346	2	B84502	probable DnaJ prot
52	45	55.6	389	2	A64202	heat shock protein
53	44	54.3	352	2	A39660	heat shock protein
54	44	54.3	373	2	F81333	chaperone DnaJ Cj1
55	44	54.3	386	2	T09709	ADP,ATP carrier pr
56	44	54.3	389	2	T44957	heat shock protein
57	44	54.3	391	2	B84207	heat shock protein
58	44	54.3	397	2	S33312	dnaJ protein - lee
59	44	54.3	413	2	S35581	dnaJ protein homol
60	44	54.3	419	2	T07371	chaperone ANJ1 pro
61	44	54.3	419	2	T07371	dnaJ protein homol
62	44	54.3	419	2	T01643	DnaJ protein homol
63	44	54.3	420	2	S71199	DnaJ protein homol
64	44	54.3	420	2	T49127	DnaJ protein homol
65	43	53.1	170	2	T09601	DnaJ protein homol
66	43	53.1	242	2	JC7933	spermatogenic cell
67	43	53.1	345	2	T08563	dnaJ-related prote
68	43	53.1	369	2	B72327	dnaJ protein - The
69	43	53.1	396	2	T06102	heat shock protein
70	42	51.9	372	2	T48660	heat shock protein
71	42	51.9	390	2	S73459	heat shock protein
72	42	51.9	392	2	D81683	dnaJ protein TC061
73	42	51.9	392	2	H71526	probable heat shoc
74	42	51.9	423	2	T43929	DnaJ protein homol
75	42	51.9	518	2	S42091	Tid(56) protein -
76	41	50.6	223	2	T12472	hypothetical prote
77	41	50.6	253	2	A97106	response regulator
78	41	50.6	302	2	T39146	hypothetical prote
79	41	50.6	349	2	B86237	protein F14N23.23
80	41	50.6	369	2	G71831	co-chaperone with
81	41	50.6	369	2	D64686	co-chaperone and h
82	41	50.6	379	2	S21313	ADP,ATP carrier pr
83	41	50.6	379	2	S55900	DNAJ-like protein
84	41	50.6	379	2	T41633	psi protein - fiss
85	41	50.6	391	2	G84611	probable DnaJ prot
86	41	50.6	418	2	S42031	LDJ2 protein - lee
87	41	50.6	423	2	T09338	DnaJ-like protein
88	41	50.6	528	2	T41362	hypothetical prote
89	41	50.6	559	2	JT0949	egg-specific prote
90	40	49.4	237	2	B82292	response regulator
91	40	49.4	241	2	B69655	two-component resp
92	40	49.4	313	2	S43888	3-isopropylmalate
93	40	49.4	356	2	E81130	3-isopropylmalate
94	40	49.4	356	2	E81836	probable 3-isoprop
95	40	49.4	385	2	D95350	probable transmemb
96	40	49.4	401	2	T18661	hypothetical prote
97	40	49.4	407	2	T39658	probable mitochond
98	40	49.4	420	2	F75396	dnaJ protein - Dei
99	40	49.4	601	1	A64222	heat shock protein
100	40	49.4	620	2	A83182	hypothetical prote

## ALIGNMENTS

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RESULT 1
HHECDJ
heat shock protein dnaJ - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A925298; S40537; G64721; A26299
R:Barwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zyllicz, M.; Georgopoulos, C.
J. Biol. Chem. 261, 1782-1785, 1986
A:Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.
A:Reference number: A92572; MUID:86111850; PMID:3003085
A:Accession: A92572
A:Molecule type: DNA
A:Residues: 1-376 <BAR>
A:Cross-references: UNIPROT:P08622; GB:M12565; NID:g145767; PIDN:AAA23693.1; PID:g145769
A:Experimental source: strain K12
R:Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.
J. Biol. Chem. 261, 1778-1781, 1986
A:Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the g
A:Reference number: A26298; MUID:86111849; PMID:3003084
A:Accession: A26298
A:Molecule type: DNA
A:Residues: 1-376 <OHK>
A:Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GB
R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu
submitted to the EMBL Data Library, December 1992
A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2
A:Reference number: S40531
A:Accession: S40537
A:Molecule type: DNA
A:Residues: 1-376 <YUR>
A:Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01292.1; PID:g216441
R:Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64721
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <BLAT>
A:Cross-references: GB:AE000112; GB:U00096; NID:g1786192; PIDN:AACT3126.1; PID:g1786197;
A:Experimental source: strain K-12, substrain MG1655
C:Comment: This protein is induced by heat shock under the control of the htpR gene prod
C:Genetics:
A:Gene: dnaJ
A:Map position: 0 min
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F:5-70/Domain: dnaJ amino-terminal homology <DNJ>
F:77-106/Region: G/F motif
F:144-151/Region: CXXCXGXG repeat
F:161-168/Region: CXXCXGXG repeat
F:183-190/Region: CXXCXGXG repeat
F:197-204/Region: CXXCXGXG repeat

Query Match 100.0%; Score 81; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 2
G90630
DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90630

Query Match 100.0%; Score 81; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 4
AF0503
DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0503
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:gi6501296; GSPDB:GN00176
```

```
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90630
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HAY>
A:Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:BA000007; PIDN:BA033438.1; PID:g1
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS0015
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 3
G85481
Chaperone with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85481
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85481
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <STO>
A:Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:AE005174; NID:g12512693; PIDN:AAG
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 4
AF0503
DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0503
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:gi6501296; GSPDB:GN00176
```



## C:Genetics:

A:Gene: STY0013

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

## RESULT 5

AB0058

Chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AB0058

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 &lt;KUR&gt;

A:Cross-references: UNIPROT:Q8ZIM6; GB:AL590842; PIDN:CAC99325.1; PID:gl5978561; GSPDB:G

## C:Genetics:

A:Gene: dnaJ

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

## RESULT 6

C64112

heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 20-Aug-1999

C:Accession: C64112

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64112

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-394 &lt;TIGR&gt;

A:Cross-references: GB:L42023; GB:U32803; NID:gl574162; PIDN:AAC22890.1; PID:gl574168; T

## C:Genetics:

A:Gene: dnaJ

A:Start codon: GTG

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F;17-82/Domain: dnaJ amino-terminal homology &lt;DNJ&gt;

F;89-121/Region: G/F motif

F;159-166/Region: CXXCXGXG repeat

F;176-183/Region: CXXCXGXG repeat

F;198-205/Region: CXXCXGXG repeat

F;212-219/Region: CXXCXGXG repeat

Query Match 100.0%; Score 81; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

|||||

Db 73 QKRAAYDQYGHAAFE 87

## RESULT 7

D82270

dnaJ protein VC0856 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: D82270

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers,

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: D82270

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 &lt;HEI&gt;

A:Cross-references: UNIPROT:O34242; GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF940

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0856

A:Map position: 1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 96.3%; Score 78; DB 2; Length 381;

Best Local Similarity 93.3%; Pred. No. 4.9e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

|||||

Db 61 QKRAAYDQYGHAAFE 75

## RESULT 8

S15295

nolC protein - Rhizobium fredii

C:Species: Rhizobium fredii

C:Date: 21-Nov-1993 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C:Accession: S15295

R;Krishnan, H.B.; Pueppke, S.G.

Mol. Microbiol. 5, 737-745, 1991

A:Title: nolC, a Rhizobium fredii gene involved in cultivar-specific nodulation of soyb

A:Reference number: S15295; MUID:91260457; PMID:1646377

A:Accession: S15295

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 &lt;MOL&gt;

A:Cross-references: UNIPROT:P26508; GB:I03521; NID:gl52353; PIDN:AAA26333.1; PID:gl5235

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F;4-69/Domain: dnaJ amino-terminal homology &lt;DNJ&gt;

Query Match 95.1%; Score 77; DB 2; Length 392;

Best Local Similarity 93.3%; Pred. No. 7.6e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

|||||

Db 60 QKRAAYDQYGHAAFE 74

## RESULT 9

P84947

dnaJ protein [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

C:Accession: F84947  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: F84947  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: dnaJ; BUL52  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 92.6%; Score 75; DB 2; Length 377;  
Best Local Similarity 86.7%; Pred. No. 1.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
:|||||  
Db 61 EKRSAYDQYGHAAFE 75

RESULT 10  
JCS609  
heat shock protein dnaJ - Buchnera sp.  
C:Species: Buchnera sp.  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: JCS609  
R:Sato, S.; Ishikawa, H.  
J. Biochem. 122, 41-48, 1997  
A:Title: Structure and expression of the dnaJ operon of Buchnera, an intracellular symbiont  
A:Reference number: JCS608; MUID:97420684; PMID:9276669  
A:Accession: JCS609  
A:Molecule type: DNA  
A:Residues: 1-377 <SAT>  
A:Cross-references: DDBJ:088673; NID:G2351215; PIDN:BAAL1965.1; PID:G2351217  
C:Comment: This protein binds to DnaK protein and GrpE protein and modulates the chaperone  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: DNA replication; heat shock; molecular chaperone  
F:5-70/Domain: dnaJ amino-terminal homology <DNJ>  
F:77-108/Region: G/F motif  
F:145-152/Region: CXXCXGXG repeat  
F:162-169/Region: CXXCXGXG repeat  
F:184-191/Region: CXXCXGXG repeat  
F:198-205/Region: CXXCXGXG repeat

Query Match 92.6%; Score 75; DB 2; Length 377;  
Best Local Similarity 86.7%; Pred. No. 1.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
:|||||  
Db 61 EKRSAYDQYGHAAFE 75

RESULT 11  
D81242  
DnaJ protein NMA0209 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: D81242; C82015  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzia, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: D81242

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-373 <TET>  
A:Cross-references: UNIPROT:P57107; GB:AE002366; GB:AE002098; NID:g7225284; PIDN:AAF4052  
A:Experimental source: serogroup B, strain MC58  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: C82015  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-373 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83522.1; PID:g737897  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: dnaJ; NMB0059; NMA0209  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 373;  
Best Local Similarity 86.7%; Pred. No. 3.7e-05;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
:|||||  
Db 61 EKRAAYDQYGHAAFE 75

RESULT 12  
B47042  
heat shock protein dnaJ - Brucella ovis  
C:Species: Brucella ovis  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B47042  
R:Cellier, M.P.; Teyssier, J.; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri Widada, J.  
J. Bacteriol. 174, 8036-8042, 1992  
A:Title: Cloning and characterization of the Brucella ovis heat shock protein DnaK function  
A:Reference number: A47042; MUID:93094135; PMID:1459952  
A:Accession: B47042  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-375 <CEL>  
A:Cross-references: UNIPROT:Q05980; EMBL:M95799; NID:g144114; PIDN:BAC36133.1; PID:g14411  
A:Note: Sequence extracted from NCBI backbone (NCBIN:119966, NCBIP:119968)  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: DNA replication; heat shock; molecular chaperone  
F:4-69/Domain: dnaJ amino-terminal homology <DNJ>  
F:76-108/Region: G/F motif  
F:146-153/Region: CXXCXGXG repeat  
F:163-170/Region: CXXCXGXG repeat  
F:185-192/Region: CXXCXGXG repeat  
F:199-206/Region: CXXCXGXG repeat

Query Match 90.1%; Score 73; DB 2; Length 375;  
Best Local Similarity 86.7%; Pred. No. 3.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15  
:|||||  
Db 60 QKRAAYDRGHAAFE 74

RESULT 13  
D97373  
chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cerson)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: D97373  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001  
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58  
 A/Reference number: A97359; MUID:21608551; PMID:11743194  
 A/Accession: D97373  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-377 <KUR>  
 A/Cross-references: UNIPROT:P50018; GB:AE007869; PIDN:AAK85941.1; PID:g15154994; GSPDB:C58  
 C/Genetics:  
 A/Gene: AGR\_C192  
 A/Map position: circular chromosome  
 C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;  
 Best Local Similarity 86.7%; Pred. No. 3.7e-05;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
 Db 61 QKRAAYDRFGHAAFE 75

RESULT 14  
 AD2591  
 molecular chaperone, DnaJ family dnaJ [imported] - *Agrobacterium tumefaciens* (strain C58)  
 C/Species: *Agrobacterium tumefaciens*  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C/Accession: AD2591  
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.  
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A/Reference number: AB2577; MUID:21608550; PMID:11743193  
 A/Accession: AD2591  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-377 <KUR>  
 A/Cross-references: UNIPROT:P50018; GB:AE008688; PIDN:AAJ41146.1; PID:g17738442; GSPDB:C58  
 A/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Gene: dnaJ  
 A/Map position: circular chromosome  
 C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;  
 Best Local Similarity 86.7%; Pred. No. 3.7e-05;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
 Db 61 QKRAAYDRFGHAAFE 75

RESULT 15  
 AC3502  
 chaperone protein dnaJ [imported] - *Brucella melitensis* (strain 16M)  
 C/Species: *Brucella melitensis*  
 C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C/Accession: AC3502  
 R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, I.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A>Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
 A/Reference number: AD3252; PMID:11756688  
 A/Accession: AC3502  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-377 <KUR>  
 A/Cross-references: UNIPROT:Q8VE77; UNIPROT:Q8FXX1; GB:AE008917; PIDN:AAJ53182.1; PID:g15154994  
 A/Experimental source: strain 16M

## C/Genetics:

A/Gene: BMEI2001

A/Map position: I

C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 3.7e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 60 QKRAAYDRFGHAAFE 74

## RESULT 16

C71729

dnaJ protein (dnaJ) RP184 - *Rickettsia prowazekii*C/Species: *Rickettsia prowazekii*

C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004

C/Accession: C71729

R/Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark,

Nature 396, 133-140, 1998

A>Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A/Reference number: A71630; MUID:99039499; PMID:9823893

A/Accession: C71729

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-370 &lt;AND&gt;

A/Cross-references: UNIPROT:Q9ZDV0; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA146

A/Experimental source: strain Madrid E

C/Genetics:

A/Gene: dnaJ; RP184

C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

P:4-68/Domain: dnaJ amino-terminal homology &lt;DNJ&gt;

Query Match 79.0%; Score 64; DB 2; Length 370;

Best Local Similarity 73.3%; Pred. No. 0.0014;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 59 QKRAAYDRFGHDAFQ 73

## RESULT 17

E70361

chaperone DnaJ - *Aquifex aeolicus*C/Species: *Aquifex aeolicus*

C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C/Accession: E70361

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'Neil,

Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: E70361

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-376 &lt;AQF&gt;

A/Cross-references: UNIPROT:O66921; GB:AE000703; NID:g2983287; PIDN:AAO6881.1; PID:g29

A/Experimental source: strain VF5

C/Genetics:

A/Gene: dnaJ2

C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:8-72/Domain: dnaJ amino-terminal homology &lt;DNJ&gt;

Query Match 77.8%; Score 63; DB 2; Length 376;

Best Local Similarity 73.3%; Pred. No. 0.0022;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 63 EKRLYDMYGHAAFE 77

```
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 RKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
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Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 RKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
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Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q92J37; GB:AE006914; PIDN:AAI02770.1; PID:gl5619285; GSPDB:G
C;Genetics:
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 74.1%; Score 60; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.0074;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDELGHDAFQ 73

RESULT 21
I40843
heat shock protein dnaJ - Coxiella burnetii
C;Species: Coxiella burnetii
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40843
R;Zuber, M.; Hoover, T.A.; Court, D.L.
Gene 152, 99-102, 1995
A;Title: Cloning, sequencing and expression of the dnaJ gene of Coxiella burnetii.
A;Reference number: I40843; MUID:95129924; PMID:7828937
A;Accession: I40843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: UNIPROT:P42381; GB:L36455; NID:g547392; PIDN:AAA65100.1; PID:G547399
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 72.8%; Score 59; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 RKRASYDQFGHAGVE 75

RESULT 22
H86902
DnaJ protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86902
R;Polotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:P35514; GB:AE005176; PID:g12725291; PIDN:AAK06322.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
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A:Gene: dnaJ  
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 71.6%; Score 58; DB 2; Length 379;  
 Best Local Similarity 91.7%; Pred. No. 0.017;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
 |||||  
 Db 60 QKRAAYDQYGEA 71

RESULT 23  
 A47079  
 heat shock protein dnaJ - Lactococcus lactis  
 C:Species: Lactococcus lactis  
 C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A47079  
 R:van Aseeldonk, M.; Simons, A.; Visser, H.; de Vos, W.M.; Simons, G.  
 J. Bacteriol. 175, 1637-1644, 1993  
 A:Title: Cloning, nucleotide sequence, and regulatory analysis of the Lactococcus lactis  
 A:Reference number: A47079; MUID:93194788; PMID:8449872  
 A:Contents: NIZO R5  
 A:Accession: A47079  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-379 <VAN>  
 A:Cross-references: UNIPROT:P35514; EMBL:M99413; NID:G293012  
 A:Experimental source: strain NIZO R5  
 A:Note: sequence extracted from NCBI backbone (NCBIN:127395, NCBIIP:127396)  
 C:Genetics:  
 A:Gene: dnaJ  
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
 C:Keywords: DNA replication; heat shock; molecular chaperone  
 F:5-69/Domain: dnaJ amino-terminal homology <DNJ>  
 F:76-114/Region: G/P motif  
 F:154-161/Region: CXXCXGXG repeat  
 F:171-178/Region: CXXCXGXG repeat  
 F:197-204/Region: CXXCXGXG repeat  
 F:211-218/Region: CXXCXGXG repeat

Query Match 71.6%; Score 58; DB 2; Length 379;  
 Best Local Similarity 91.7%; Pred. No. 0.017;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
 |||||  
 Db 60 QKRAAYDQYGEA 71

RESULT 24  
 C87250  
 dnaJ protein [imported] - Caulobacter crescentus  
 C:Species: Caulobacter crescentus  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C:Accession: C87250  
 R:Nierman, W.C.; Feldblym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eise, J.; Heidelberg, J.  
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of Caulobacter crescentus.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: C87250  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-385 <STO>  
 A:Cross-references: UNIPROT:P22305; GB:AE005673; NID:G13421099; PIDN:AAK21999.1; GSPDB:G  
 C:Genetics:  
 A:Gene: CC0011

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 71.6%; Score 58; DB 2; Length 385;  
 Best Local Similarity 83.3%; Pred. No. 0.017;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
 |||||  
 Db 59 QKRAAYDRFGHA 70

RESULT 25  
 A49210  
 heat shock protein dnaJ - Lyme disease spirochete  
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Aug-1998  
 C:Accession: A49210  
 R:Anzola, J.; Luft, B.J.; Gorgone, G.; Peltz, G.  
 Infect. Immun. 60, 4965-4968, 1992  
 A:Title: Characterization of a Borrelia burgdorferi dnaJ homolog.  
 A:Reference number: A49210; MUID:93014224; PMID:1383161  
 A:Accession: A49210  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-352 <ANZ>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:116537, NCBIIP:116539)  
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
 F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.4%; Score 57; DB 2; Length 352;  
 Best Local Similarity 64.3%; Pred. No. 0.024;  
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15  
 |||||  
 Db 61 KKAKYDRFGHSAFE 74

RESULT 26  
 D70164  
 heat shock protein dnaJ-1 - Lyme disease spirochete  
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
 C:Accession: D70164; S30946  
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt  
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A:Authors: Smith, H.O.; Venter, J.C.  
 A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A:Reference number: A70100; MUID:98065943; PMID:9403685  
 A:Accession: D70164  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-364 <KLB>  
 A:Cross-references: UNIPROT:P28616; GB:AE001154; GB:AE000783; NID:G2688431; PIDN:AAC668

A:Experimental source: strain B31  
 R:Fillly, K.; Hauser, R.; Campbell, J.; Oestheimer, G.J.  
 Mol. Microbiol. 7, 359-369, 1993  
 A:Title: Isolation of dnaJ, dnaK, and grpE homologues from Borrelia burgdorferi and cor  
 A:Reference number: S30944; MUID:93211279; PMID:8459764  
 A:Accession: S30946  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-364 <TIL>  
 A:Cross-references: EMBL:M96847  
 C:Genetics:  
 A:Start codon: GTG  
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
 F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.4%; Score 57; DB 2; Length 364;  
 Best Local Similarity 64.3%; Pred. No. 0.025;  
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15  
 |||||

Db 61 KKAKYDRFGHSAFE 74

RESULT 27  
AD1621  
heat shock protein dnaJ [imported] - *Listeria innocua* (strain Clip11262)  
C:Species: *Listeria innocua*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD1621  
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1621  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <GLA>  
A:Cross-references: UNIPROT:Q985A3; GB:AL592022; PIDN:CAC96740.1; PID:g16413982; GSPDB:G  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 70.4%; Score 57; DB 2; Length 376;  
Best Local Similarity 90.9%; Pred. No. 0.025;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
|||||  
Db 60 QKRAQYDQYGH 70

RESULT 28  
T43739  
heat shock protein dnaJ [imported] - *Listeria monocytogenes*  
C:Species: *Listeria monocytogenes*  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T43739  
R:Hanawa, T.; Kai, M.; Kamiya, S.; Yamamoto, T.  
submitted to the EMBL Data Library, February 1999  
A:Description: Cloning, sequencing, and transcriptional analysis of the dnaK heat shock  
A:Reference number: Z22656  
A:Accession: T43739  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-377 <HAN>  
A:Cross-references: UNIPROT:Q9SSA3; EMBL:AB023064; PIDN:BAA82790.1  
A:Experimental source: strain 10403S  
C:Genetics:  
A:Note: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: molecular chaperone; stress-induced protein  
F;S-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.4%; Score 57; DB 2; Length 377;  
Best Local Similarity 90.9%; Pred. No. 0.026;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
|||||  
Db 60 QKRAQYDQYGH 70

RESULT 29  
AH1258  
heat shock protein dnaJ [imported] - *Listeria monocytogenes* (strain EGD-e)  
C:Species: *Listeria monocytogenes*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AH1258

R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1258  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <GLA>  
A:Cross-references: UNIPROT:Q985A3; GB:NC\_003210; PIDN:CAC99550.1; PID:g16410901; GSPDB:G  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 70.4%; Score 57; DB 2; Length 377;  
Best Local Similarity 90.9%; Pred. No. 0.026;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
|||||  
Db 60 QKRAQYDQYGH 70

RESULT 30  
F82570  
DnaJ protein XP2339 [imported] - *Xylella fastidiosa* (strain 9a5c)  
C:Species: *Xylella fastidiosa*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82570  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below

A:Accession: F82570  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-368 <STM>  
A:Cross-references: UNIPROT:Q9PB06; GB:AE004044; GB:AE003849; NID:g9107501; PIDN:AAF8513  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XP2339  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 368;  
Best Local Similarity 66.7%; Pred. No. 0.037;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|||:-|||  
Db 61 KKRKLYDTHGHAAFE 75

RESULT 31  
H97928

heat-shock protein (activation of DnaK) [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: H97928  
R:Hookins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: H97928  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-372 <KUR>  
A:Cross-references: UNIPROT:Q8CWT2; GB:AE007317; PIDN:AAK99260.1; PID:G15458025; GSPDB:G  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 372;  
Best Local Similarity 91.7%; Pred. No. 0.038;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
| | | | | | | | | | | | | | | |  
Db 60 QKRAAYDQYGA 71

RESULT 32  
D95060  
dnaJ protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95060  
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, P.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: D95060  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-378 <KUR>  
A:Cross-references: UNIPROT:P95830; GB:AE005672; PIDN:AAK74677.1; PID:G14971993; GSPDB:G  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0519  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 69.1%; Score 56; DB 2; Length 378;  
Best Local Similarity 91.7%; Pred. No. 0.038;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
| | | | | | | | | | | | | | | |  
Db 60 QKRAAYDQYGA 71

RESULT 33  
G96831  
hypothetical protein F18B13.12 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G96831  
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: G96831  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-499 <STO>  
A:Cross-references: UNIPROT:Q9SSD4; GB:AE005173; NID:G5902381; PIDN:AAD55483.1; GSPDB:G  
C:Genetics:  
A:Gene: F18B13.12  
A:Map position: 1  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 65.4%; Score 53; DB 2; Length 499;  
Best Local Similarity 83.3%; Pred. No. 0.17;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
| | | | | | | | | | | | | | | |  
Db 130 QKRAAYDQYGE 141

RESULT 34  
B41874  
heat shock protein dnaJ - Bacillus subtilis  
C:Species: Bacillus subtilis  
C>Date: 03-May-1994 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: B41874; S09501; G69617; S27506  
R:Wetzelstein, M.; Voelker, U.; Dedio, J.; Loebau, S.; Zuber, U.; Schiesswohl, M.; Herget  
J. Bacteriol. 174, 3300-3310, 1992  
A:Title: Cloning, sequencing, and molecular analysis of the dnaK locus from Bacillus su  
A:Reference number: A41874; MUID:92250426; PMID:1339421  
A:Accession: B41874  
A:Molecule type: DNA  
A:Residues: 1-372 <WET>  
A:Cross-references: UNIPROT:PI7631; EMBL:M84964; NID:G143056; PIDN:AAA22529.1; PID:G143  
R:Wetzelstein, M.; Dedio, J.; Schumann, W.  
Nucleic Acids Res. 18, 2172, 1990  
A:Title: Complete nucleotide sequence of the Bacillus subtilis dnaK gene.  
A:Reference number: S09500; MUID:90245667; PMID:2110662  
A:Accession: S09501  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-24 <WET>  
A:Cross-references: EMBL:X52064; NID:G93888; PIDN:CAA36287.1; PID:G93890  
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koster, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parto, V.; Pohl, T.M.; Portetelli  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, F.; Tognoni, J.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: G9617  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-372 <KUN>  
A:Cross-references: GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14488.1; PID:G2634992  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein



F:5-69/Domain: dnaJ amino-terminal homology <DNJ>  
F:76-105/Region: G/F motif  
F:145-152/Region: CXXCXGXG repeat  
F:162-169/Region: CXXCXGXG repeat  
F:188-195/Region: CXXCXGXG repeat  
F:202-209/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 372;  
Best Local Similarity 81.8%; Pred. No. 0.19;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
:|||||:|:|  
Db 60 QKRAHYDQFGH 70

## RESULT 35

H69038  
heat shock protein dnaJ - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: H69038  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func0  
A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: H69038

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-376 <MTH>

A:Cross-references: UNIPROT:O27352; GB:AE000894; GB:AE000666; NID:g2622392; PIDN:AAB8577

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: WTH1291

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone

F:5-69/Domain: dnaJ amino-terminal homology <DNJ>

F:75-111/Region: G/F motif

F:148-155/Region: CXXCXGXG repeat

F:165-172/Region: CXXCXGXG repeat

F:191-198/Region: CXXCXGXG repeat

F:205-212/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 376;  
Best Local Similarity 53.3%; Pred. No. 0.2;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|||||:|:|  
Db 60 EKRAHYDQFGHAGMD 74

## RESULT 36

S41748  
heat shock protein dnaJ - Methanosarcina mazei  
C:Species: Methanosarcina mazei  
C:Date: 31-Dec-1993 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: S41748; S41150  
R:Conway de Macario, E.  
submitted to the EMBL Data Library, April 1992

A:Reference number: S41748

A:Accession: S41748

A:Molecule type: DNA

A:Residues: 1-389 <CON>

A:Cross-references: UNIPROT:P35515; EMBL:X60265; NID:g48938; PIDN:CAA42813.1; PID:g48940

A:Experimental source: strain S-6

R:Macario, A.J.L.; Dugan, C.B.; Clarens, M.; Conway de Macario, E.

Nucleic Acids Res. 21, 2773, 1993

A:Title: dnaJ in Archaea.

A:Reference number: S41150; MUID:93324351; PMID:8332479

A:Accession: S41150

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 4-208 <MAC>

A:Cross-references: EMBL:X60265; NID:g48938; PIDN:CAA42813.1; PID:g48940

A:Experimental source: strain S-6

C:Genetics:

A:Gene: dnaJ

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:6-70/Domain: dnaJ amino-terminal homology <DNJ>

F:77-104/Region: G/F motif

F:144-151/Region: CXXCXGXG repeat

F:161-168/Region: CXXCXGXG repeat

F:187-194/Region: CXXCXGXG repeat

F:201-208/Region: CXXCXGXG repeat

Query Match 64.2%; Score 52; DB 2; Length 389;  
Best Local Similarity 53.3%; Pred. No. 0.2;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|||||:|:|  
Db 61 EKRAQYDRFGHAGID 75

## RESULT 37

GB1329  
probable curved-DNA binding protein Cj1229 [imported] - Campylobacter jejuni (strain NCTC

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: GB1329

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: AB1250; MUID:20150912; PMID:10688204

A:Accession: GB1329

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-297 <PAR>

A:Cross-references: UNIPROT:Q9PN68; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7348

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: cbpA; Cj1229

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 297;  
Best Local Similarity 64.3%; Pred. No. 0.35;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAAF 14  
:|||||:|:|  
Db 58 KKRAQYDQYGDMSMF 71

## RESULT 38

T04618  
heat shock protein homolog F2009.160 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04618  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, October 1998

A:Reference number: Z15380

A:Accession: T04618

A:Molecule type: DNA

A:Residues: 1-348 <BEV>

A:Cross-references: UNIPROT:O49457; EMBL:AL021749

A:Experimental source: cultivar Columbia; BAC clone F2009

C:Genetics:

A:Map position: 4

A:Introns: 55/3; 204/2

A>Note: F2009.160



C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F:4-70/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 61.7%; Score 50; DB 2; Length 348;  
Best Local Similarity 90.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYQG 10  
|||||  
Db 61 QKRAVYDOYG 70

## RESULT 39

B89939  
DnaJ protein [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: B89939  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: B89939  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-379 <KUR>  
A:Cross-references: UNIPROT:Q99TR8; GB:BA000018; PID:gl3701377; PIDN:BAB42671.1; GSPDB:C  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 379;  
Best Local Similarity 80.0%; Pred. No. 0.45;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDOYGH 11  
|||||  
Db 61 KRAVYDOYGH 70

## RESULT 40

E90603  
heat shock protein dnaJ (activation of DNak) [imported] - Mycoplasma pulmonis (strain UA  
C:Species: Mycoplasma pulmonis  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: E90603  
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallieson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
A:Reference number: A99512; MUID:21267165; PMID:11353084  
A:Accession: E90603  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-383 <KUR>  
A:Cross-references: UNIPROT:Q98PI9; GB:AL445566; PID:gl4090148; PIDN:CAC13906.1; GSPDB:C  
A:Experimental source: strain UAB CT1P  
C:Genetics:  
A:Gene: MYPV\_7330  
A:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 61.7%; Score 50; DB 2; Length 383;  
Best Local Similarity 61.5%; Pred. No. 0.45;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGHAA 13  
:|:|:|:|:|  
Db 67 EKRAVYDOYGH 79

## RESULT 41

F71379  
heat shock protein dnaJ - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 28-Aug-1998 #sequence\_revision 28-Aug-1998 #text\_change 17-Mar-1999  
C:Accession: F71379  
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McC  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876  
A:Accession: F71379  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-416 <COL>  
A:Cross-references: GB:AE001203; GB:AE000520; NID:g33222476  
A:Experimental source: strain Nichols  
A:Note: This ORF is annotated but not translated in GenBank entry AE001203, release 107  
C:Comment: This is the hypothetical translation of a sequence that was reported as a co  
C:Comment: This translation was produced by PIR staff from information in the GenBank a  
ion codon. A BLAST search of the GenBank database shows that, in the majority of cases,  
C:Genetics:  
A:Gene: TP0217  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein; t  
F:48-113/Domain: dnaJ amino-terminal homology <DNJ>  
F:325-326/Region: plus-two translational frameshift

Query Match 61.7%; Score 50; DB 2; Length 416;  
Best Local Similarity 90.0%; Pred. No. 0.49;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYQG 10  
|||||  
Db 104 QKRAAYDRYG 113

## RESULT 42

D83818  
heat-shock protein (activation of DnaK) dnaJ [imported] - Bacillus halodurans (strain C  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: D83818  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: D83818  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-370 <STO>  
A:Cross-references: UNIPROT:Q9KD71; GB:AP001511; GB:BA000004; NID:gl0173727; PIDN:BA05  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 60.5%; Score 49; DB 2; Length 370;  
Best Local Similarity 72.7%; Pred. No. 0.65;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDOYGH 11  
||:|:|:|:|  
Db 60 QKRAHYDQFGH 70

## RESULT 43

D82894  
heat shock protein UU407 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: D82894

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.  
submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A:Reference number: A82870  
A:Accession: D82894  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-375 <GLA>  
A:Cross-references: GB:AE002138; GB:AF222894; NID:g6899390; PIDN:AAF30818.1; GSPDB:GN001  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: dnaJ; U0407  
A:Genetic code: SGC3  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 60.5%; Score 49; DB 2; Length 375;  
Best Local Similarity 72.7%; Pred. No. 0.66; Mismatches 2; Indels 1; Gaps 0;  
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGH 11  
: ||| ||| :  
Db 59 KKRQYDQGH 69  
: ||| ||| :  
: ||| ||| :  
: ||| ||| :

RESULT 44  
T06594  
heat shock protein dnaJ - garden pea  
C:Species: Pisum sativum (garden pea)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06594  
R;Schlacher, T.; Soll, J.  
submitted to the EMBL Data Library, July 1997  
A:Description: DnaJ and GrpE homologues in pea chloroplasts.  
A:Reference number: Z15784  
A:Accession: T06594  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-498 <SCH>  
A:Cross-references: UNIPROT:P92424; EMBL:Z71640; PIDN:CAA96305.1  
A:Experimental source: var. Golf  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: chloroplast; heat shock; stress-induced protein  
F:71-135/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 60.5%; Score 49; DB 2; Length 498;  
Best Local Similarity 75.0%; Pred. No. 0.89; Mismatches 1; Indels 2; Gaps 0;  
Matches 9; Conservative 1; Mismatches 1; Indels 2; Gaps 0;

QY 1 QKRAAYDQYGH 12  
: ||| ||| :  
Db 126 KKRQYDQGEA 137  
: ||| ||| :  
: ||| ||| :  
: ||| ||| :

RESULT 45  
JC4739  
heat shock protein dnaJ - Bacillus stearothermophilus  
C:Species: Bacillus stearothermophilus  
C:Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: JC4739  
R;Herbert, M.; Schoen, U.; Angermann, K.; Lang, J.; Schumann, W.  
Gene 170, 81-84, 1996  
A:Title: Cloning and sequencing of the dnaK operon of Bacillus stearothermophilus.  
A:Reference number: JC4738; MUID:96200860; PMID:8621094  
A:Accession: JC4739  
A:Molecule type: DNA  
A:Residues: 1-380 <HER>  
A:Cross-references: UNIPROT:Q45552; EMBL:X90709; NID:g1568471; PIDN:CAA62240.1; PID:g156  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:5-69/Domain: dnaJ amino-terminal homology <DNJ>  
F:76-108/Region: G/F motif  
F:148-155/Region: CXXCXGXG repeat  
F:165-172/Region: CXXCXGXG repeat  
F:191-198/Region: CXXCXGXG repeat  
F:205-212/Region: CXXCXGXG repeat

Query Match 59.3%; Score 48; DB 2; Length 380;  
Best Local Similarity 75.0%; Pred. No. 1; Mismatches 1; Indels 2; Gaps 0;  
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 QKRAAYDQYGH 12  
: ||| ||| :  
Db 60 QKRAHYDQFGA 71  
: ||| ||| :  
: ||| ||| :  
: ||| ||| :

RESULT 46  
S29852  
ADP,ATP carrier protein - Arabidopsis thaliana  
N:Alternate names: adenine nucleotide translocator  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S29852; S29618  
R;Schuster, W.; Kloek, S.; Brennicke, A.  
Biochim. Biophys. Acta 1172, 205-208, 1993  
A:Title: An adenine nucleotide translocator gene from Arabidopsis thaliana.  
A:Reference number: S29852; MUID:93176813; PMID:8439563  
A:Accession: S29852  
A:Molecule type: DNA  
A:Residues: 1-385 <SCH>  
A:Cross-references: UNIPROT:P40941; EMBL:X68592; NID:g16159; PIDN:CAA48579.1; PID:g16160  
C:Genetics:  
A:Gene: ANT2  
A:Introns: 162/3; 287/3  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C:Keywords: duplication; mitochondrion; transmembrane protein  
F:81-176/Domain: ADP,ATP carrier protein repeat homology <ACPL>  
F:186-281/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:287-375/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 59.3%; Score 48; DB 1; Length 385;  
Best Local Similarity 60.0%; Pred. No. 1; Mismatches 2; Indels 4; Gaps 0;  
Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 1 QKRAAYDQYGH 15  
: ||| ||| :  
Db 41 QKHAAYGNYSNAFQ 55  
: ||| ||| :  
: ||| ||| :  
: ||| ||| :

RESULT 47  
S73361  
dnaJ homolog protein C09\_orf910 - Mycoplasma pneumoniae (strain ATCC 29342)  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: S73361  
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73361  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-910 <HIM>  
A:Cross-references: UNIPROT:P75354; EMBL:AE000004; GB:U00089; NID:g1673671; PIDN:AAB9568  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Genetic code: SGC3  
A:Superfamily: Mycoplasma heat shock protein dnaJ homolog C09\_orf910; dnaJ amino-terminal  
F:7-71/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 59.3%; Score 48; DB 1; Length 910;  
Best Local Similarity 72.7%; Pred. No. 2.5;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 11  
:|||||

Db 62 KRAYNDYKIGH 72

RESULT 48  
G84590  
probable heat shock protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G84590  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: G84590  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-337 <STO>  
A;Cross-references: UNIPROT:Q9SIL3; GB:A8002093; NID:94586038; PIDN:AAD25656.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g20560  
A;Map position: 2  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 58.0%; Score 47; DB 2; Length 337;  
Best Local Similarity 80.0%; Pred. No. 1.3;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 10  
:|||||

Db 61 OKRAAYDOYGH 70

RESULT 49  
S38898  
heat shock protein MDJ1 precursor - yeast (Saccharomyces cerevisiae)  
N;Alternate names: MDJ1 protein; protein YFL016C  
C;Species: Saccharomyces cerevisiae  
C;Date: 31-Dec-1993 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S38898; S48320; A53500; S56238; S62297  
R;Rowley, N.K.; Prip-Buus, C.; Westermann, B.; Brown, C.M.; Schwarz, E.; Barrell, B.G.;  
submitted to the EMBL Data Library, November 1993  
A;Description: Mdj1p, a novel DnaJ homologue of Saccharomyces cerevisiae, plays a role in  
A;Reference number: S38898  
A;Accession: S38898  
A;Molecule type: DNA  
A;Residues: 1-511 <ROW>  
A;Cross-references: UNIPROT:P35191; EMBL:Z28336; NID:9431909; PIDN:CAA82189.1; PID:94319  
R;Churcher, C.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S48310  
A;Accession: S48320  
A;Molecule type: DNA  
A;Residues: 1-511 <CHU>  
A;Cross-references: EMBL:Z46255; NID:9559925; PIDN:CAA86351.1; PID:G559936; MIPS:YFL016C  
R;Rowley, N.; Prip-Buus, C.; Westermann, B.; Brown, C.; Schwarz, E.; Barrell, B.; Neuph  
Cell 77, 249-259, 1994  
A;Title: Mdj1p, a novel chaperone of the DnaJ family, is involved in mitochondrial bioge  
A;Reference number: A53500; MUID:94221642; PMID:8168133  
A;Accession: A53500  
A;Molecule type: DNA  
A;Residues: 1-511 <RO2>  
A;Cross-references: GB:Z28336; NID:9431909; PIDN:CAA82189.1; PID:9431910  
R;Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasam  
submitted to the EMBL Data Library, May 1995  
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce  
A;Reference number: S56186  
A;Accession: S56238

A;Molecule type: DNA  
A;Residues: 1-511 <MUR>  
A;Cross-references: EMBL:D50617; NID:9836685; PIDN:BAA09222.1; PID:9836738; MIPS:YFL016C  
R;Murakami, Y.  
submitted to the EMBL Data Library, December 1994  
A;Reference number: S62230  
A;Accession: S62297  
A;Molecule type: DNA  
A;Residues: 1-511 <MUW>  
A;Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08001.1; PID:g1100788  
C;Genetics:  
A;Gene: SGD:MDJ1  
A;Cross-references: SGD:S0001878; MIPS:YFL016C  
A;Map position: 6L  
A;Genome: nuclear  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C;Keywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion;  
F;1-55/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F;56-511/Product: heat shock protein MDJ1 #status predicted <MAT>  
F;61-125/Domain: dnaJ amino-terminal homology <DNU>

Query Match 58.0%; Score 47; DB 2; Length 511;  
Best Local Similarity 69.2%; Pred. No. 2.1;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRAAYDOYGHAAF 14  
:|||||

Db 117 KROQYDQFGPAAP 129

RESULT 50  
T48161  
heat shock protein 40-like - Arabidopsis thaliana  
N;Alternate names: protein T1008.100  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48161  
R;Bevan, M.; Pohl, T.; Weizensegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24486  
A;Accession: T48161  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-335 <BEV>  
A;Cross-references: UNIPROT:Q5M034; EMBL:AL161746  
A;Experimental source: cultivar Columbia; BAC clone T1008  
C;Genetics:  
A;Map position: 5  
A;Introns: 55/3; 190/2  
A;Note: T1008.100  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;4-70/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 55.6%; Score 45; DB 2; Length 335;  
Best Local Similarity 80.0%; Pred. No. 3;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 10  
:|||||

Db 61 OKRAAYEQYGH 70

RESULT 51  
B84602  
probable DnaJ protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84602  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Title: Characterization of SIS1, a Saccharomyces cerevisiae homologue of bacterial dna  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: B84602  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-346 <STO>  
A;Cross-references: UNIPROT:Q9SUS8; GB:AE002093; NID:g4567282; PIDN:AAD23695.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g21510  
A;Map position: 2

Query Match 55.6%; Score 45; DB 2; Length 346;  
Best Local Similarity 88.9%; Pred. No. 3.1;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYG 10  
Db 63 KRAAYDKYG 71

RESULT 52  
A64202  
heat shock protein dnaJ - Mycoplasma genitalium  
C;Species: Mycoplasma genitalium  
C;Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: A64202; T09677  
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A;Title: The minimal gene complement of Mycoplasma genitalium.  
A;Reference number: A64200; MUID:196026346; PMID:7569993  
A;Accession: A64202  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-389 <TIGR>  
A;Cross-references: UNIPROT:P47265; GB:U39680; GB:L43967; NID:g1045681; PID:g1045688; TI  
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merrick  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z16818  
A;Accession: T09677  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-389 <FRA>  
A;Cross-references: EMBL:U39681; NID:g3844626; PID:g3844628  
A;Experimental source: isolate G37  
C;Genetics:  
A;Gene: MG019  
A;Genetic code: SGC3  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C;Keywords: molecular chaperone  
F;7-77/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 55.6%; Score 45; DB 2; Length 389;  
Best Local Similarity 63.6%; Pred. No. 3.5;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGH 11  
Db 68 EKRLDYDQFGH 78

RESULT 53  
A39660  
heat shock protein SIS1 - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein N2879; protein YNL007c  
C;Species: Saccharomyces cerevisiae  
C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004  
C;Accession: A39660; S62918; S17003; S19042  
R;Luke, M.M.; Sutton, A.; Arndt, K.T.  
J. Cell Biol. 114, 623-638, 1991

A;Title: Characterization of SIS1, a Saccharomyces cerevisiae homologue of bacterial dna  
A;Reference number: A39660; MUID:91332100; PMID:1714460  
A;Accession: A39660  
A;Molecule type: DNA  
A;Residues: 1-352 <LUK>  
A;Cross-references: UNIPROT:P25294; GB:X58460; NID:g4473; PIDN:CAA41366.1; PID:g4474  
R;Doignon, F.; Crouzet, M.  
submitted to the Protein Sequence Database, April 1996  
A;Reference number: S62916  
A;Accession: S62918  
A;Molecule type: DNA  
A;Residues: 1-352 <DOI>  
A;Cross-references: EMBL:Z71283; NID:g1301823; PIDN:CAA95866.1; PID:g1301824; MIPS:YNL00  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:SIS1  
A;Cross-references: SGD:S0004952; MIPS:YNL007c  
A;Map position: 14L  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C;Keywords: dimer; DNA binding; heat shock; stress-induced protein  
F;6-68/Domain: dnaJ amino-terminal homology <DNJ>  
F;141-166/Region: glycine/methionine-rich

Query Match 54.3%; Score 44; DB 2; Length 352;  
Best Local Similarity 80.0%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OKRAAYDQYG 10  
Db 59 OKREIYDQYG 68

RESULT 54  
F81333  
chaperone DnaJ Cj1260c [imported] - Campylobacter jejuni (strain NCTC 11168)  
C;Species: Campylobacter jejuni  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: F81333  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chillin  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: F81333  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-373 <PAR>  
A;Cross-references: UNIPROT:O85213; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7351  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: dnaJ; Cj1260c  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 54.3%; Score 44; DB 2; Length 373;  
Best Local Similarity 53.3%; Pred. No. 5.1;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15  
Db 60 EKRAIYDRYKDKALK 74

RESULT 55  
T09709  
ADP,ATP carrier protein CANT1 - upland cotton  
N;Alternate names: adenine nucleotide translocator 1  
C;Species: Gossypium hirsutum (upland cotton)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09709  
R;Shin, H.; Brown, R.M.  
submitted to the EMBL Data Library, June 1997  
A;Reference number: Z16832  
A;Accession: T09709

A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 1-386 <SHI>  
A;Cross-references: UNIPROT:O22342; EMBL:AF006489; NID:g2463663; PID:g2463664  
A;Experimental source: strain Texas marker1; fiber  
C;Genetics:  
A;Gene: CANT1  
C;Function:  
A;Description: catalyzes the exchange of ADP and ATP  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
P;188-282/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match 54.3%; Score 44; DB 2; Length 386;  
Best Local Similarity 53.3%; Pred. No. 5.3;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
|:|||||:|:|:  
Db 40 QKRAAYGNYSNAALQ 54  
|:|||||:|:|:

RESULT 56  
T44957  
heat shock protein dnaJ [similarity] - Halobacterium salinarum (ATCC 33170)  
N;Alternate names: 40K chaperone; 40K heat shock protein  
C;Species: Halobacterium salinarum  
A;Variety: ATCC 33170  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T44957  
R;Bustard, K.; Gupta, R.S.  
J. Mol. Evol. 45, 193-205, 1997  
A;Title: The sequences of heat shock protein 40 (DnaJ) homologs provide evidence for a d  
A;Reference number: 222880; MUID:97383250; PMID:9236279  
A;Accession: T44957  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: DNA  
A;Residues: 1-389 <BUS>  
A;Cross-references: UNIPROT:O34135; EMBL:U93357; PIDN:AAB96891.1  
A;Experimental source: ATCC 33170  
A;Note: the source is designated as Halobacterium cutirubrum  
C;Genetics:  
A;Gene: dnaJ  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;4-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 389;  
Best Local Similarity 53.3%; Pred. No. 5.3;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
|:|||||:|:|:  
Db 59 ETRQQYDQLGHERFE 73  
|:|||||:|:|:

RESULT 57  
E84207  
heat shock protein [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E84207  
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: E84207  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-391 <STO>  
A;Cross-references: UNIPROT:Q9HRY3; GB:A8004437; NID:g10580095; PIDN:AAG19025.1; GSPDB:G  
C;Genetics:

A;Gene: dnaJ  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 54.3%; Score 44; DB 2; Length 391;  
Best Local Similarity 53.3%; Pred. No. 5.3;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
|:|||||:|:|:  
Db 59 ETRQQYDQLGHERFE 73  
|:|||||:|:|:

RESULT 58  
S33312  
dnaJ protein - leek (fragment)  
C;Species: Allium porrum (leek)  
C;Date: 06-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S33312; S31387  
R;Bessoule, J.J.  
FEBS Lett. 323, 51-54, 1993  
A;Title: Occurrence and sequence of a DnaJ protein in plant (Allium porrum) epidermal c  
A;Reference number: S33312; MUID:93265942; PMID:8495747  
A;Accession: S33312  
A;Molecule type: mRNA  
A;Residues: 1-397 <BES>  
A;Cross-references: UNIPROT:Q03363; EMBL:X69436; NID:g16086; PIDN:CAA49211.1; PID:g1608  
C;Genetics:  
A;Gene: dnaJ  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;1-53/Domain: dnaJ amino-terminal homology (fragment) <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 397;  
Best Local Similarity 53.3%; Pred. No. 5.4;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
|:|||||:|:|:  
Db 44 EKREIYDQYGEDALK 58  
|:|||||:|:|:

RESULT 59  
S35581  
dnaJ protein homolog DnaJ-1 - cucumber  
C;Species: Cucumis sativus (cucumber)  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: S35581; S31414  
R;Preisig-Mueller, R.; Kindl, H.  
Arch. Biochem. Biophys. 305, 30-37, 1993  
A;Title: Plant dnaJ homologue: molecular cloning, bacterial expression, and expression  
A;Reference number: S35581; MUID:93343632; PMID:8342953  
A;Accession: S35581  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-413 <PRE1>  
A;Cross-references: UNIPROT:Q04960; EMBL:X67695  
R;Preisig-Mueller, R.; Kindl, H.  
submitted to the EMBL Data Library, August 1992  
A;Description: Plant equivalent of a nuclear localization sequence-binding protein. Hig  
A;Reference number: S31414  
A;Accession: S31414  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-223, 'V', 225-239, 'A', 241-302, 'P', 304-377, 379-380, 'V', 381-413 <PRE2>  
A;Cross-references: EMBL:X67695; NID:g18259; PIDN:CAA47925.1; PID:g18260  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;12-73/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 413;  
Best Local Similarity 53.3%; Pred. No. 5.6;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
|:|||||:|:|:

Db 64 EKREIYDQYGEDALK 78

RESULT 60

JQ2142

Chaperone ANU1 protein - Atriplex nummularia

C:Species: Atriplex nummularia

C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004

C:Accession: JQ2142

R:Zhu, J.K.; Shi, J.; Bressan, R.A.; Hasegawa, P.M.

Plant Cell 5, 341-349, 1993

A:Title: Expression of an Atriplex nummularia gene encoding a protein homologous to the

A:Reference number: JQ2142; M0ID:93222693; PMID:8467224

A:Accession: JQ2142

A:Molecule type: mRNA

A:Residues: 1-417 <ZHU>

A:CROSS-references: UNIPROT:P43644; GB:I09124

C:Comment: This protein is involved in protein folding and is observed as heat shock pro

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 417;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 61

T07371

dnaJ protein homolog - potato

C:Species: Solanum tuberosum (potato)

C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004

C:Accession: T07371

R:Leggiewie, G.; Braun, H.P.

Plant Physiol. 117, 1127, 1998

A:Title: A cDNA from potato with homology to DnaJ is identical to a hitherto unidentified

A:Reference number: Z15992

A:Accession: T07371

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-419 <LEG>

A:CROSS-references: UNIPROT:Q43177; EMBL:X94301; NID:g1125690; PIDN:CAA63965.1

A:Experimental source: tissue type leaf

C:Genetics:

A:Gene: dnaJ

A>Note: induced upon tuberization

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 419;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 62

T01643

DnaJ protein homolog ZMDJ1 - maize

C:Species: Zea mays (maize)

C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004

C:Accession: T01643

R:Baszczynski, C.L.; Barbour, E.; Zeka, B.; Maddock, S.E.; Swenson, J.L.

Maydica 42, 189-201, 1997

A:Title: Characterization of a genomic clone for a maize DnaJ-related gene, ZmdJ1, and e

A:Reference number: Z14364

A:Accession: T01643

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-419 <BAS>

A:CROSS-references: UNIPROT:O65160; EMBL:AF053468; NID:g2984708; PIDN:AAC08009.1; PID:g2

C:Genetics:

A:Gene: mdj1

A:Introns: 50/3; 105/1; 153/2; 245/3; 312/1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; molecular chaperone

F:13-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 419;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 65 EKREIYDQYGEDALK 79

RESULT 63

S71199

dnaJ protein homolog atj3 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C:Accession: S71199

R:Zhou, R.; Kroczyńska, B.; Miernyk, J.A.

submitted to the EMBL Data Library, March 1995

A:Description: AtJ3, an Arabidopsis thaliana homologue of the Escherichia coli DnaJ.

A:Reference number: S71199

A:Accession: S71199

A:Molecule type: mRNA

A:Residues: 1-420 <ZHO>

A:CROSS-references: UNIPROT:Q42530; EMBL:U22340; NID:gi872162; PIDN:AAB49030.1; PID:g727

C:Genetics:

A:Gene: atj3

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:14-75/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 420;

Best Local Similarity 53.3%; Pred. No. 5.7;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 66 EKREIYDQYGEDALK 80

RESULT 64

T49127

dnaJ protein homolog atj3 - Arabidopsis thaliana

N:Alternate names: protein F26G5.60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C:Accession: T49127

R:P'Angelio, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25017

A:Accession: T49127

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-420 <DAN>

A:CROSS-references: UNIPROT:O22663; EMBL:AL33814; GSPDB:GN00061; ATSP:F26G5.60

A:Experimental source: cultivar Columbia; BAC clone F26G5

C:Genetics:

A:Gene: ATSP:F26G5.60

A:Map position: 3

A:Introns: 51/3; 107/1; 153/2; 245/3; 312/1

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F:14-75/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 54.3%; Score 44; DB 2; Length 420;

Best Local Similarity 53.3%; Pred. No. 5.7;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
DB 66 EKREIYDQYGDALK 80

RESULT 65  
T09601  
DnaJ protein homolog - alfalfa (fragment)  
C/Species: Medicago sativa (alfalfa)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T09601  
R/Frugis, G.  
submitted to the EMBL Data Library, April 1996  
A/Description: Isolation of an alfalfa DnaJ-like gene and a Y13 proteasome subunit homolog  
A/Reference number: Z16763  
A/Accession: T09601  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-170 <FRU>  
A/Cross-references: UNIPROT:Q24075; EMBL:Z71997  
A/Experimental source: variety Rangelsander; non-embryogenic callus  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C/Keywords: molecular chaperone

Query Match 53.1%; Score 43; DB 2; Length 170;  
Best Local Similarity 46.7%; Pred. No. 3.4;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
DB 4 EKREIYDQYGDALK 18

RESULT 66  
JC7933  
spermatogenic cell-specific DnaJ-like protein, MFSJ1 protein - Japanese macaque  
C/Species: Macaca fuscata (Japanese macaque)  
C/Date: 22-Jun-2003 #sequence\_revision 22-Jun-2003 #text\_change 07-Jul-2003  
C/Accession: JC7933  
R/Yu, S.S.; Takenaka, O.  
Biochem. Biophys. Res. Commun. 301, 443-449, 2003  
A/Title: Molecular cloning, structure, and testis-specific expression of MFSJ1, a member of the DnaJ family  
A/Reference number: JC7933; MUID:22452769; PMID:12565881  
A/Accession: JC7933  
A/Molecule type: mRNA  
A/Residues: 1-242 <YUA>  
A/Cross-references: DDBJ:AB095737  
C/Comment: This protein is a testis-specific DnaJ-like protein. It acts together with the DnaJ family proteins to regulate spermatogenesis.  
C/Genetics:  
A/Gene: mfpj1  
C/Keywords: DnaJ-like protein; spermatogenesis; testis-specific

Query Match 53.1%; Score 43; DB 2; Length 242;  
Best Local Similarity 53.3%; Pred. No. 4.9;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
DB 60 KKRVDYDRYGEAGAE 74

RESULT 67  
T08563  
dnaJ-related protein T22F8.50 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: T08563  
R/Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16442  
A/Accession: T08563  
A/Molecule type: DNA  
A/Residues: 1-345 <BEV>  
A/Cross-references: UNIPROT:Q9T024; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.50  
A/Experimental source: cultivar Columbia; BAC clone T22F8  
C/Genetics:  
A/Gene: ATSP:T22F8.50  
A/Map position: 4  
A/Introns: 29/3; 49/3; 77/2; 132/3; 176/1; 229/1; 286/3; 313/3  
F:6-71/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 345;  
Best Local Similarity 70.0%; Pred. No. 7;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 10  
DB 62 EKRTAYDKYG 71

RESULT 68  
B72327  
dnaJ protein - Thermotoga maritima (strain MSB8)  
C/Species: Thermotoga maritima  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: B72327  
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.R.; Nelson, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.  
Nature 399, 323-329, 1999  
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing  
A/Reference number: A72200; MUID:99287316; PMID:10360571  
A/Accession: B72327  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-369 <ARN>  
A/Cross-references: UNIPROT:Q9WZV3; GB:AE001751; GB:AE000512; NID:94981371; PIDN:AAD359  
A/Experimental source: strain MSB8  
C/Genetics:  
A/Gene: TM0849  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F:7-73/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 369;  
Best Local Similarity 63.6%; Pred. No. 7.5;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 11  
DB 64 QKRAAYDRFGY 74

RESULT 69  
T06102  
heat shock protein T5J17.130, dnaJ-type - Arabidopsis thaliana  
N/Alternate names: protein T5J17.130  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T06102  
R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
submitted to the Protein Sequence Database, March 1999  
A/Reference number: Z15184  
A/Accession: T06102  
A/Molecule type: DNA  
A/Residues: 1-396 <BEV>  
A/Cross-references: UNIPROT:Q9SMQ9; EMBL:AL035708; GSPDB:GN00062; ATSP:T5J17.130  
A/Experimental source: cultivar Columbia; BAC clone T5J17  
C/Genetics:  
A/Gene: ATSP:T5J17.130  
A/Map position: 4  
A/Introns: 33/3; 53/1; 67/2; 83/3; 111/3  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; stress-induced protein  
F:34-98/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 53.1%; Score 43; DB 2; Length 396;  
Best Local Similarity 58.3%; Pred. No. 8.1;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGH 12  
: ||| : ||| : |||  
DB 89 EKRSYLDYRGEA 100

## RESULT 70

T48660  
heat shock protein dnaJ [validated] - Campylobacter jejuni

N:Alternate names: chaparone DnaJ  
C:Species: Campylobacter jejuni  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: T48660  
R:Konkel, M.E.; Kim, B.J.; Klena, J.D.; Young, C.R.; Ziprin, R.  
Infect. Immun. 66, 3666-3672, 1998  
A:Title: Characterization of the thermal stress response of campylobacter jejuni.  
A:Reference number: Z24513; MUID:98339866; PMID:9673247  
A:Accession: T48660  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-372 <KON>  
A:Cross-references: UNIPROT:O85213; EMBL:AF052661; NID:g3435158; PIDN:AAC32328.1; PID:g3435158  
A:Experimental source: strain F38011  
C:Genetics:  
A:Gene: dnaJ  
C:Function:

A:Description: aids in bacteriophage replication [validated, MUID:98339866]

A:Note: elevated expression after heat shock

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: heat shock; molecular chaperone

F:4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 372;  
Best Local Similarity 70.0%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQY 10  
: ||| : ||| : |||

DB 60 EKRAIYDRYG 69

## RESULT 71

S73459  
heat shock protein DnaJ - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: hypothetical protein D12 orf390  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S73459  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73459  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-390 <HIM>  
A:Cross-references: UNIPROT:P78004; EMBL:AE000015; GB:U00089; NID:g1673779; PIDN:AAB9578  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: dnaJ  
A:Genetic code: SGC3  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F:7-77/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 51.9%; Score 42; DB 2; Length 390;  
Best Local Similarity 54.5%; Pred. No. 12;

QY 1 QKRAAYDQYGH 11  
: ||| : ||| : |||

DB 68 EKRCMYDRFGH 78

## RESULT 72

D81683  
dnaJ protein TC0619 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: D81683  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: D81683  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-392 <TET>  
A:Cross-references: UNIPROT:Q9PK53; GB:AE002330; GB:AE002160; NID:g7190649; PIDN:AAF3945  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0619  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 51.9%; Score 42; DB 2; Length 392;  
Best Local Similarity 70.0%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQY 10  
: ||| : ||| : |||

DB 58 QKRESYDRYG 67

## RESULT 74

T43929  
DnaJ protein homolog [imported] - Salix gilgiana

C:Species: Salix gilgiana  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T43929

Query Match 51.9%; Score 42; DB 2; Length 392;  
Best Local Similarity 70.0%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQY 10  
: ||| : ||| : |||

DB 58 QKRESYDRYG 67

## RESULT 74

T43929  
DnaJ protein homolog [imported] - Salix gilgiana

C:Species: Salix gilgiana  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T43929

Query Match 51.9%; Score 42; DB 2; Length 392;  
Best Local Similarity 70.0%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQY 10  
: ||| : ||| : |||

DB 58 QKRESYDRYG 67



R;Putamura, N.; Ishii-Minami, N.; Hayaashida, N.; Shinohara, K.  
Plant Cell Physiol. 40, 524-531, 1999  
A;Title: Expression of DnaJ homologs and Hep70 in the Japanese Willow (*Salix gilgiana* Se  
A;Reference number: Z22726; MUID:99356782; PMID:10427775  
A;Accession: T43929  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-423 <FUT>  
A;Cross-references: UNIPROT:Q9SYX7; EMBL:AB003137; PIDN:BAA76883.1  
C;Species: *Drosophila melanogaster*  
C;Date: 06-Jan-1995 #sequence\_revision 1; Mismatches 5; Indels 0; Gaps 0;  
F;13-74/Domain: dnaJ amino-terminal homology <DNJ>  
Query Match 51.9%; Score 42; DB 2; Length 423;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 KRAAYDQYGHAAFE 15  
Db 66 KREIYDQYGEDALK 79  
RESULT 75  
S42091  
Tid(56) protein - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
A;Accession: S42091  
R;Kurzik-Dumke, U.; Gundacker, D.; Rentrop, M.; Gateff, E.  
submitted to the EMBL Data Library, February 1994  
A;Description: Tumor suppression in *Drosophila* is causally related to the function of th  
A;Reference number: S42091  
A;Accession: S42091  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-518 <KUR>  
A;Cross-references: UNIPROT:Q27237; EMBL:X77822; NID:G2511642; PID:G456627  
C;Genetics:  
A;Gene: FlyBase:l(2)tid  
A;Cross-references: FlyBase:FBgn0002174  
A;Introns: 443/2  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;63-128/Domain: dnaJ amino-terminal homology <DNJ>  
Query Match 51.9%; Score 42; DB 2; Length 518;  
Best Local Similarity 61.5%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 KRAAYDQYGHAA 13  
Db 119 QKRREYDTYGQTA 131  
RESULT 76  
T12472  
hypothetical protein DKFZp564F1862.1 - human  
C;Species: *Homo sapiens* (man)  
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T12472  
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A;Reference number: Z17526  
A;Accession: T12472  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-223 <BLU>  
A;Cross-references: UNIPROT:Q9UBS3; EMBL:AL080081  
A;Experimental source: fetal brain; clone DKFZp564F1862  
C;Genetics:  
A;Note: DKFZp564F1862.1  
F;26-90/Domain: dnaJ amino-terminal homology <DNJ>  
Query Match 50.6%; Score 41; DB 2; Length 223;  
Best Local Similarity 53.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 KRAAYDQYGHAAFP 14  
Db 82 RRKEYDTLGHSAF 94  
RESULT 77  
A97106  
response regulator (Chev-like receiver domain and DNA-binding HTH domain) [imported] -  
C;Species: *Clostridium acetobutylicum*  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 15-Sep-2003  
C;Accession: A97106  
R;Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
; Daly, M.J.; Bennett, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: A97106  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-253 <KUR>  
A;Cross-references: GB:AB001437; PIDN:AAK79636.1; PID:G15024631; GSPDB:GN00168  
C;Experimental source: *Clostridium acetobutylicum* ATCC824  
C;Genetics:  
A;Gene: CAC1670  
C;Superfamily: response regulator with LysR DNA-binding domain, Algr/VirK/COME type; r  
Query Match 50.6%; Score 41; DB 2; Length 253;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 AYDQYGHAAFE 15  
Db 84 AYDKYAAVAAP 94  
RESULT 78  
T39146  
hypothetical protein SPAC8C9.09c - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T39146  
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21748  
A;Accession: T39146  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-302 <OLI>  
A;Cross-references: UNIPROT:O14278; EMBL:Z99168; PIDN:CAB16297.1; GSPDB:GN00066; SPDB:5  
A;Experimental source: strain 972h; cosmid c8C9  
C;Genetics:  
A;Gene: SPDB:SPAC8C9.09c  
A;Map position: 1  
Query Match 50.6%; Score 41; DB 2; Length 302;  
Best Local Similarity 57.1%; Pred. No. 14;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 OKRAAYDQYGHAAFP 14  
Db 154 RXEALSKLGHAPF 167  
RESULT 79  
E86237  
protein F14N23.23 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E86237  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: E86237  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <STO>  
A;Cross-references: UNIPROT:Q9SY77; GB:AE005172; NID:g4914337; PIDN:AAD32885.1; GSPDB:GN  
C;Genetics:  
A;Map position: 1  
A;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 50.6%; Score 41; DB 2; Length 349;  
Best Local Similarity 70.0%; Pred. NO. 16;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
:|:|:|:|:|:|  
Db 61 QRRQIYDQYG 70

RESULT 80  
G71831  
co-chaperone with dnaK - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: G71831  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: G71831  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-369 <ARN>  
A;Cross-references: UNIPROT:Q9ZJ02; GB:AE001548; GB:AE001439; NID:g4155845; PIDN:AAD0682  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: dnaJ\_2  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 369;  
Best Local Similarity 70.0%; Pred. NO. 17;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
:|:|:|:|:|:|  
Db 60 KKRALYDRYG 69

RESULT 81  
D64686  
co-chaperone and heat shock protein - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: D64686  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
A;Reference number: A64520; MUID:9739467; PMID:9252185

A;Accession: D64686  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-369 <TOM>  
A;Cross-references: UNIPROT:O25890; GB:AE000634; GB:AE000511; NID:g2314489; PIDN:AAD0837  
C;Genetics:  
A;Start codon: GTG  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 369;  
Best Local Similarity 70.0%; Pred. NO. 17;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10  
:|:|:|:|:|:|  
Db 60 KKRALYDRYG 69

RESULT 82  
S21313  
ADP, ATP carrier protein - Arabidopsis thaliana (fragment)  
N;Alternate names: adenine nucleotide translocator  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S21313  
R;Saint-Gully, A.; Poh-Yam, L.; Chevalier, C.; Yamaguchi, J.; Akazawa, T.  
submitted to the EMBL Data Library, April 1992  
A;Reference number: S21313  
A;Accession: S21313  
A;Molecule type: mRNA  
A;Residues: 1-379 <SAI>  
A;Cross-references: UNIPROT:P31167; EMBL:X65549; NID:g16174; PIDN:CAA46518.1; PID:g16175  
C;Genetics:  
A;Gene: ANTI  
C;Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
C;Keywords: duplication; mitochondrion; transmembrane protein  
F;75-170/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
F;180-275/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
F;281-369/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 50.6%; Score 41; DB 2; Length 379;  
Best Local Similarity 46.7%; Pred. NO. 18;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
:|:|:|:|:|:|  
Db 36 QRHATYGNYSNAAFQ 50

RESULT 83  
S55900  
DNAJ-like protein homolog - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: Schizosaccharomyces pombe  
C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S55900  
R;Park, S.K.; Chon, S.K.; Yoo, H.S.  
Biochim. Biophys. Acta 1262, 87-90, 1995  
A;Title: A cDNA of *Schizosaccharomyces pombe* encoding a homologue of DnaJ-like protein.  
A;Reference number: S55900; MUID:95290501; PMID:7772606  
A;Accession: S55900  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-379 <PAR>  
A;Cross-references: UNIPROT:Q09912; EMBL:L37753; NID:g576932; PIDN:AAA74732.1; PID:g99532  
C;Genetics:  
A;Gene: psi  
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
F;6-68/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 379;  
Best Local Similarity 70.0%; Pred. NO. 18;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
 Db 59 QRRKLYDQYG 68

## RESULT 84

T41633  
 psi protein - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 R/McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.  
 submitted to the EMBL Data Library, August 1999  
 A/Reference number: Z22005  
 A/Accession: T41633  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-379 <MCD>  
 A/Cross-references: UNIPROT:Q09912; EMBL:AL109850; PIDN:CAB52880.1; GSPDB:GN00068; SPDB:  
 A/Experimental source: strain 972h; cosmid c830  
 C/Genetics:  
 A/Gene: SPDB:SPCC830.07C  
 A/Map position: 3  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
 euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197  
 A/Accession: G84611  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-391 <STO>  
 A/Cross-references: UNIPROT:Q9SJZ7; GB:AB002093; NID:94544454; PIDN:AAD22362.1; GSPDB:GN  
 C/Genetics:  
 A/Gene: At2g22360  
 A/Map position: 2  
 C/Species: Allium porrum (leek)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 A/Accession: S42031

Query Match 50.6%; Score 41; DB 2; Length 379;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 F/6-68/Domain: dnaJ amino-terminal homology <DNJ>

Qy 1 QKRAAYDQYG 10  
 Db 59 QRRKLYDQYG 68

## RESULT 85

G84611  
 probable DnaJ protein [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
 euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197  
 A/Accession: G84611  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-391 <STO>  
 A/Cross-references: UNIPROT:Q9SJZ7; GB:AB002093; NID:94544454; PIDN:AAD22362.1; GSPDB:GN  
 C/Genetics:  
 A/Gene: At2g22360  
 A/Map position: 2  
 C/Species: Allium porrum (leek)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 A/Accession: S42031

Query Match 50.6%; Score 41; DB 2; Length 391;  
 Best Local Similarity 40.0%; Pred. No. 18;  
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
 Db 90 EKSLYDQYGEAGLK 104

## RESULT 86

S42031  
 LDJ2 protein - leek  
 C/Species: Allium porrum (leek)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 A/Accession: S42031

R/Bessoule, J.J.; Testet, B.; Cassagne, C.  
 submitted to the EMBL Data Library, February 1994  
 A/Reference number: S42031  
 A/Accession: S42031  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-418 <BES>  
 A/Cross-references: UNIPROT:P42824; EMBL:X77632; NID:9454913; PIDN:CAA54720.1; PID:9454  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 R/McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.  
 submitted to the EMBL Data Library, August 1999  
 A/Reference number: Z22005  
 A/Accession: T41633  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-379 <MCD>  
 A/Cross-references: UNIPROT:Q09912; EMBL:AL109850; PIDN:CAB52880.1; GSPDB:GN00068; SPDB:  
 A/Experimental source: strain 972h; cosmid c830  
 C/Genetics:  
 A/Gene: SPDB:SPCC830.07C  
 A/Map position: 3  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
 euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197  
 A/Accession: G84611  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-391 <STO>  
 A/Cross-references: UNIPROT:Q9SJZ7; GB:AB002093; NID:94544454; PIDN:AAD22362.1; GSPDB:GN  
 C/Genetics:  
 A/Gene: At2g22360  
 A/Map position: 2  
 C/Species: Allium porrum (leek)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 A/Accession: S42031

Query Match 50.6%; Score 41; DB 2; Length 418;  
 Best Local Similarity 70.0%; Pred. No. 19;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYG 10  
 Db 65 EKREIYDQYG 74

## RESULT 87

T09338  
 DnaJ-like protein MeJ1 - alfalfa  
 C/Species: Medicago sativa (alfalfa)  
 C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
 R/Erugis, G.; Mele, G.; Giannino, D.; Mariotti, D.  
 submitted to the EMBL Data Library, June 1998  
 A/Description: Isolation and characterization of a DnaJ-like gene from alfalfa.  
 A/Reference number: Z16649  
 A/Accession: T09338  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-423 <FRU>  
 A/Cross-references: UNIPROT:O24074; EMBL:AF069507; NID:G3202019; PID:G3202020  
 C/Genetics:  
 A/Gene: MeJ1  
 A/Intons: 51/3; 108/1; 155/2; 200/1; 247/3; 314/1  
 C/Suprafamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
 F/4-15/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 50.6%; Score 41; DB 2; Length 423;  
 Best Local Similarity 46.7%; Pred. No. 20;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15  
 Db 66 EKRELYDQYGEDALK 80

## RESULT 88

T41362  
 hypothetical protein SPCC4G3.14 - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 05-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.  
 submitted to the EMBL Data Library, March 1998  
 A/Reference number: Z21918  
 A/Accession: T41362  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-528 <WOO>  
 A/Cross-references: UNIPROT:P87239; EMBL:Z97052; PIDN:CAB09769.1; GSPDB:GN00068; SPDB:  
 A/Experimental source: strain 972h; cosmid c4G3  
 C/Genetics:  
 A/Gene: SPDB:SPCC4G3.14  
 A/Map position: 3  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 A/Accession: S42031

Query Match 50.6%; Score 41; DB 2; Length 528;  
 Best Local Similarity 46.7%; Pred. No. 25;

Matches	7;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	QKRAAYDQYGHAAFE 15							
DB	141	KKKKAFDTYAGAFK 155							
		: : : : : :							
RESULT 89									
JT0949									
egg-specific protein - silkworm									
C:Species: Bombyx mori (silkworm)									
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004									
C:Accession: JT0949; A28527									
R:Sato, Y.; Yamashita, O.									
submitted to JIPID, September 1991									
A:Reference number: JT0949									
A:Accession: JT0949									
A:Molecule type: DNA									
A:Residues: 1-559 <SAT>									
A:Cross-references: UNIPROT:Q17219									
A:Experimental source: larva									
A>Note: this protein is a homotrimer									
R:Indrasith, L.S.; Sasaki, T.; Yamashita, O.									
J. Biol. Chem. 263, 1045-1051, 1988									
A:Title: A unique protease responsible for selective degradation of a yolk protein in <i>B. mori</i>									
A:Reference number: A28527; MUID:88087166; PMID:3275655									
A:Accession: A28527									
A:Molecule type: protein									
A:Residues: 19-40;133-144, 'T', 146-152;229-248 <IND>									
C:Genetics:									
A:Map position: 19									
C:Keywords: egg yolk; homotrimer									
F:132-133/Cleavage site: Lys-Asn (egg 30.5K cysteine proteinase) #status experimental									
F:228-229/Cleavage site: Arg-Asp (egg 30.5K cysteine proteinase) #status experimental									
Query Match	50.6%	Score 41;	DB 2;	Length 559;					
Best Local Similarity	70.0%;	Pred. No. 26;							
Matches	7;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
QY	6	YDQYGHAAFE 15							
DB	382	HDQVGHGAFA 391							
		: : : : : :							
RESULT 90									
B82292									
response regulator VC0693 [imported] - Vibrio cholerae (strain N16961 serogroup O1)									
C:Species: Vibrio cholerae									
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004									
C:Accession: B82292									
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;									
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.									
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.									
Nature 406, 477-483, 2000									
A:Title: DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> .									
A:Reference number: A82035; MUID:20406833; PMID:10952301									
A:Accession: B82292									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-237 <HRI>									
A:Cross-references: UNIPROT:Q9KU36; GB:AB004155; GB:AB003952; NID:G9655127; PIDN:AAF9385									
A:Experimental source: serogroup O1; strain N16961; biotype El Tor									
C:Genetics:									
A:Gene: VC0693									
A:Map position: 1									
C:Superfamily: response regulator with <i>LytTR</i> DNA-binding domain, <i>AlgR/VirR/ComE</i> type; res									
Query Match	49.4%	Score 40;	DB 2;	Length 237;					
Best Local Similarity	72.7%;	Pred. No. 16;							
Matches	8;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	5	AYDQYGHAAFE 15							
		: : : : : :			</				

Db 46 AYDEYGH 52

RESULT 93

E81130

3-isopropylmalate dehydrogenase NMB1031 [imported] - Neisseria meningitidis (strain MC58)

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: E81130

C;Tectelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vitti, A.; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: E81130

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-356 <TET>

A;Cross-references: UNIPROT:Q9JZ19; GB:AE002453; GB:AE002098; NID:G7226261; PIDN:AAF4143

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB1031

C;Superfamily: 3-isopropylmalate dehydrogenase

Query Match 49.4%; Score 40; DB 2; Length 356;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AYDQYGH 11

Db 46 AYDEYGH 52

RESULT 94

E81836

probable 3-isopropylmalate dehydrogenase (EC 1.1.1.85) NMA1456 [imported] - Neisseria meningitidis

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C;Accession: E81836

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, N. Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:2022556; PMID:10761919

A;Accession: E81836

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-356 <PAR>

A;Cross-references: UNIPROT:Q9JU79; GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CAB8469

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA1454; NMA1456

C;Superfamily: 3-isopropylmalate dehydrogenase

C;Keywords: oxidoreductase

Query Match 49.4%; Score 40; DB 2; Length 356;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AYDQYGH 11

Db 46 AYDEYGH 52

RESULT 95

D95350

probable transmembrane transport protein Sma1301 [imported] - Sinorhizobium meliloti (strain 1021)

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C;Accession: D95350

R;Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95350

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-385 <KUR>

A;Cross-references: UNIPROT:Q9Z204; GB:AE006469; PIDN:AAK65366.1; PID:gl4523826; GSPDB: A;Experimental source: strain 1021, megaplasmid pSymA

R;Gallibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

C;Genetics:

A;Gene: Sma1301

A;Genome: plasmid

C;Superfamily: probable antibiotic resistance protein yybF

Query Match 49.4%; Score 40; DB 2; Length 385;

Best Local Similarity 57.1%; Pred. No. 27;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAF 14

Db 199 QKRAAYDQYGHAAF 212

RESULT 96

T18661

hypothetical protein B0035.14 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T18661

R;White, S. Submitted to the EMBL Data Library, May 1996

A;Reference number: Z19002

A;Accession: T18661

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-401 <WIL>

A;Cross-references: UNIPROT:Q17439; EMBL:Z73102; PIDN:CAA97416.1; GSPDB:GN00022; CESP: B0035

A;Experimental source: clone B0035

C;Genetics:

A;Gene: CESP:B0035.14

A;Map position: 4

A;Introns: 22/3; 47/1; 180/1; 233/1; 310/2; 365/1

Query Match 49.4%; Score 40; DB 2; Length 401;

Best Local Similarity 66.7%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAA 13

Db 193 KRRQYDQYGHAA 204

RESULT 97

T39658

probable mitochondrial protein import protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004

C;Accession: T39658

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, October 1998

A;Reference number: Z21868

A;Accession: T39658

A;Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-407 <LYN>  
A:Cross-references: UNIPROT:074752; EMBL:AL031856; PIDN:CAA21305.1; GSPDB:GN000067; SPDB:  
C:Genetics:  
A:Gene: dnaJ  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
C:Keywords: mitochondrion  
F:6-68/Domain: dnaJ amino-terminal homology <DNJ>  
Query Match 49.4%; Score 40; DB 2; Length 407;  
Best Local Similarity 40.0%; Pred. No. 28;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYGHAAFE 15  
:|||||:|:|:  
Db 59 EKRAYDREGEGQLQ 73  
:|||||:|:|:  
RESULT 98  
F75396  
dnaJ protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: F75396  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma  
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: F75396  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-420 <WHI>  
A:Cross-references: GB:AE001987; GB:AE000513; NID:g6459180; PIDN:AAF10994.1; PID:g645918  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRI424  
A:Map position: 1  
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology  
Query Match 49.4%; Score 40; DB 2; Length 420;  
Best Local Similarity 58.3%; Pred. No. 29;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYGHAA 12  
:|||||:|:|:  
Db 101 EKRAYDREGSAA 112  
:|||||:|:|:  
RESULT 99  
A64222  
heat shock protein dnaJ homolog MG200 - Mycoplasma genitalium  
C:Species: Mycoplasma genitalium  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: A64222; T09695  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A:Title: The minimal gene complement of Mycoplasma genitalium.  
A:Reference number: A64200; MUID:96026346; PMID:7569993  
A:Accession: A64222  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-601 <TIGR>  
A:Cross-references: UNIPROT:P47442; GB:U39697; GB:I43967; NID:g1045878; PID:g1045885; TI  
A:Experimental source: strain G-37  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merrick  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z16818

A:Accession: T09695  
A:Status: preliminary; translated from GB/EMBL/DBDJB  
A:Molecule type: DNA  
A:Residues: 1-601 <FRA>  
A:Cross-references: EMBL:U39699; NID:g3844790; PID:g3844797  
A:Experimental source: isolate G37  
C:Genetics:  
A:Gene: MG200  
A:Genetic code: SGC3  
C:Superfamily: Mycoplasma heat shock protein dnaJ homolog MG200; dnaJ amino-terminal hom  
C:Keywords: molecular chaperone  
F:7-71/Domain: dnaJ amino-terminal homology <DNJ>  
Query Match 49.4%; Score 40; DB 1; Length 601;  
Best Local Similarity 70.0%; Pred. No. 43;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYG 10  
:|||||:|:|:  
Db 62 KKRANYDKYG 71  
:|||||:|:|:  
RESULT 100  
A83182  
hypothetical protein PA3713 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: A83182  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A83182  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-620 <STO>  
A:Cross-references: UNIPROT:Q9HXS8; GB:AE004790; GB:AE004091; NID:g9949873; PIDN:AAG0710  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: PA3713  
Query Match 49.4%; Score 40; DB 2; Length 620;  
Best Local Similarity 58.3%; Pred. No. 44;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 4 AAYDQYGHAAFE 15  
:|||||:|:|:  
Db 599 AAWDAYAAID 610  
:|||||:|:|:  
Search completed: September 2, 2005, 20:55:40  
Job time : 18 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 2, 2005, 20:44:11 ; Search time 56 Seconds  
(without alignments)  
137.164 Million cell updates/sec

Title: US-09-616-247-4

Perfect score: 81  
Sequence: 1 OKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	372	2	Q7N8Y3 photorhabdu
2	81	100.0	375	1	DNAJ_ECOLI
3	81	100.0	376	2	Q7UDU1 shigella fl
4	81	100.0	376	2	Q8FLC5 escherichia
5	81	100.0	376	2	Q8XA65 escherichia
6	81	100.0	377	1	DNAJ_HAEDU
7	81	100.0	378	1	DNAJ_SALTY
8	81	100.0	379	2	Q8L3D3 colwellia m
9	81	100.0	379	2	Q6E8S9 yersinia ps
10	81	100.0	379	2	Q75WD2 acetobacter
11	81	100.0	379	2	Q8ZIM6 yersinia pe
12	81	100.0	379	2	Q6D0B8 erwinia car
13	81	100.0	382	1	DNAJ_HABIN
14	81	100.0	386	2	Q83MH4 shigella fl
15	78	96.3	375	1	DNAJ_ACTAC
16	78	96.3	380	2	Q6LUA6 vibrio chol
17	78	96.3	381	1	DNAJ_VIBCH
18	78	96.3	381	2	Q87RX2 vibrio para
19	78	96.3	381	2	Q8DF67 vibrio vuln
20	78	96.3	385	1	DNAJ_VIBHA
21	78	96.3	386	2	Q7MN84 vibrio vuln
22	78	96.3	389	2	Q65U54 manheimia
23	77	95.1	234	1	DNAJ_RHILE
24	77	95.1	331	2	Q93S23 rhizobium l
25	77	95.1	379	2	Q92T07 rhizobium t
26	77	95.1	392	1	NOLC_RHIFR
27	75	92.6	372	1	DNAJ_PASMU
28	75	92.6	377	1	DNAJ_BUCAI
29	74	91.4	378	1	DNAJ_BUCAP
30	73	90.1	373	1	DNAJ_NEIMA
31	73	90.1	373	1	DNAJ_NEIMB

32	73	90.1	375	1	DNAJ_BRUOV	Q05980 brucella ov
33	73	90.1	376	2	Q98DD2	Q98dd2 rhizobium l
34	73	90.1	377	1	DNAJ_AGR5	P50018 agrobacteri
35	73	90.1	377	1	DNAJ_BRUME	Q8ye77 brucella me
36	73	90.1	377	1	DNAJ_BRUSU	Q8fxx1 brucella su
37	73	90.1	379	2	Q6RSN5	Q6rsn5 agrobacteri
38	73	90.1	380	2	Q6GIF8	Q6gif8 bartonella
39	73	90.1	381	2	Q6G553	Q6g553 bartonella
40	72	88.9	379	1	DNAJ_RHOPA	Q6ncv3 rhodopseudo
41	72	88.9	379	1	DNAJ_RHOSH	Q08356 rhodopseudo
42	72	88.9	384	2	Q8R567	Q8r567 thermoaer
43	70	86.4	377	2	Q7VQL3	Q7vql3 candidatus
44	70	86.4	379	1	DNAJ_PASHA	Q52065 pasteurella
45	70	86.4	383	1	DNAJ_BUCBP	Q89au7 buchnera ap
46	69	85.2	382	2	Q8KYX6	Q8kyx6 uncultured
47	69	85.2	384	1	DNAJ_RHOCA	Q52702 rhodobacter
48	68	84.0	370	1	DNAJ_ERYRH	Q05646 erysipeloth
49	68	84.0	377	1	DNAJ_BRAJA	P94319 bradyrhizob
50	67	82.7	371	1	DNAJ_METSS	Q9zfc5 methylovoru
51	67	82.7	376	2	Q62HD6	Q62hd6 burkholderi
52	67	82.7	376	2	Q63R47	Q63r47 burkholderi
53	66	81.5	383	1	DNAJ_LACSK	Q87778 lactobacill
54	66	81.5	386	2	Q93R26	Q93r26 tetragenoco
55	65	80.2	374	2	Q8D2Q6	Q8d2q6 wigglsworth
56	64	79.0	370	1	DNAJ_RICPR	Q9zdy0 rickettsia
57	64	79.0	370	2	Q68XI3	Q68xi3 rickettsia
58	64	79.0	392	2	Q8RH03	Q8rh03 fusbacteri
59	64	79.0	393	2	Q7P753	Q7p753 fusbacteri
60	63	77.8	367	2	Q6SET1	Q6set1 uncultured
61	63	77.8	369	2	Q6SGG2	Q6sgg2 uncultured
62	63	77.8	373	2	Q7WGI5	Q7wgi5 bordetella
63	63	77.8	376	1	DNJ2_AQUAE	Q66921 aquifex aeo
64	63	77.8	377	2	Q7W520	Q7w520 bordetella
65	63	77.8	379	1	DNAJ_LEGPN	P50025 legionella
66	63	77.8	385	2	Q7VVY3	Q7vvy3 bordetella
67	62	77.8	389	2	Q835R5	Q835r5 enterococcu
68	62	76.5	376	2	Q6VAY5	Q6vay5 pseudomonas
69	62	76.5	377	1	DNAJ_PSEAE	Q9hv44 pseudomonas
70	62	76.5	380	2	Q87WP1	Q87wp1 pseudomonas
71	61	75.3	374	2	Q6F150	Q6f150 mesoplasma
72	61	75.3	387	2	Q8XIT1	Q8xiti1 clostridium
73	61	75.3	394	2	Q70WY6	Q70wy6 fusbacteri
74	60	74.1	373	2	Q7PAY0	Q7pay0 rickettsia
75	60	74.1	373	2	Q92J37	Q92j37 rickettsia
76	60	74.1	375	2	Q8PMA9	Q8pma9 xanthomonas
77	60	74.1	376	2	Q8APF2	Q8apf2 xanthomonas
78	60	74.1	376	2	Q8PAK8	Q8pak8 xanthomonas
79	60	74.1	391	2	Q7UM96	Q7um96 rhodopirell
80	59	72.8	374	1	DNAJ_CXBU	P42381 coxiella bu
81	59	72.8	375	2	Q7NXI1	Q7nxi1 chromobacte
82	59	72.8	380	2	Q8XW41	Q8xw41 ralatonia s
83	58	71.6	375	2	Q88DU3	Q88du3 pseudomonas
84	58	71.6	379	1	DNAJ_LACLA	P35514 lactococcus
85	58	71.6	379	2	Q93Q66	Q93q66 lactococcus
86	58	71.6	385	1	DNAJ_CAUCR	P22305 caulobacter
87	58	71.6	386	2	Q67S53	Q67s53 symbiobacte
88	58	71.6	414	2	Q7S1F9	Q7s1f9 neurospora
89	58	71.6	456	2	Q8LEU4	Q8leu4 arabidopsis
90	57	70.4	188	2	Q8NK58	Q8nk58 paracoccidi
91	57	70.4	364	1	DNAJ_BORBU	P28616 borrelia bu
92	57	70.4	364	2	Q661A4	Q661a4 borrelia ga
93	57	70.4	367	2	Q6Q8U1	Q6q8u1 uncultured
94	57	70.4	369	1	DNAJ_NITEU	Q06431 nitrosomona
95	57	70.4	371	2	Q634M8	Q634m8 bacillus ce
96	57	70.4	371	2	Q6MNG0	Q6mng0 bdellovibri
97	57	70.4	371	2	Q730M2	Q730m2 bacillus ce
98	57	70.4	371	2	Q818F0	Q818f0 bacillus ce
99	57	70.4	371	2	Q81LS3	Q81ls3 bacillus an
100	57	70.4	371	2	Q6HDK8	Q6hdk8 bacillus th

ALIGNMENTS

```

RESULT 1
Q7N8Y3
ID Q7N8Y3 PRELIMINARY; PRT; 372 AA.
AC Q7N8Y3;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Heat shock protein dnaJ (HSP40) (Chaperone protein).
GN Name=dnaJ; OrderedLocusNames=plu0580;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Dauchin A., Kunst F.;
RA "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RT Nat. Biotechnol. 21:1307-1313(2003).
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX571860; CAE12875.1; -.
DR HSP; P08622; 1BQZ.
DR PhotoList; plu0580; -.
DR GO; GO:0051082; F:unfolding protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 372 AA; 40820 MW; B2F36918CC6E9B1A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 9,8e-06;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 61 OKRAAYDQYGHAAFE 75
|||||
|||||

RESULT 2
DnaJ_ECOLI
ID DnaJ_ECOLI STANDARD; PRT; 375 AA.
AC P08622;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Chaperone protein dnaJ (Heat shock protein J) (HSP40).

```

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GN Name=dnaJ; Synonyms=grpP; OrderedLocusNames=b0015;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RX MEDLINE=86111849; PubMed=3003084;
RA Ohki M., Tamura F., Nishimura S., Uchida H.;
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and
RL purification of the gene product.";
RL J. Biol. Chem. 261:1778-1781(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86111850; PubMed=3003085;
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M.,
RA Georgopoulos C.;
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A
RL gene that encodes a heat shock protein.";
RL J. Biol. Chem. 261:1782-1785(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RL 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP POSSIBLE FUNCTION
RX MEDLINE=91187894; PubMed=1826368;
RA Liberek K., Marszalek J., Ang D., Georgopoulos C., Zylicz M.;
RT "Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate
RL ATPase activity of DnaK.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
RN [6]
RP STRUCTURE BY NMR OF 1-107.
RX MEDLINE=96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
RA Pellechia M., Szyperski T., Wall D., Georgopoulos C., Wuthrich K.;
RT "NMR structure of the J-domain and the Gly/Phe-rich region of the
RL Escherichia coli DnaJ chaperone.";
RL J. Mol. Biol. 260:236-250(1996).
RN [7]
RP STRUCTURE BY NMR OF 1-104.
RX MEDLINE=99224904; PubMed=10210198;
RA Huang K., Flanagan J.M., Prestegard J.H.;
RT "The influence of C-terminal extension on the structure of the 'J-
RL domain' in E. coli DnaJ.";
RL Protein Sci. 8:203-214(1999).
RN [8]
RP STRUCTURE BY NMR OF 130-208.
RX MEDLINE=20351465; PubMed=10891270; DOI=10.1006/jmbi.2000.3923;
RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
RT "Solution structure of the cysteine-rich domain of the Escherichia
RL coli chaperone protein DnaJ.";
RL J. Mol. Biol. 300:805-818(2000).
CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
CC the phage lambda origin of replication. Stimulates, jointly with
CC grpE, the ATPase activity of dnaK.
CC -!- COFACTOR: Binds 2 zinc ions per monomer.
CC -!- SUBUNIT: Homodimer.

```



CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- INDUCTION: By heat shock under the control of the htpR regulatory  
CC protein.  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
CC -!- SIMILARITY: Contains 1 CR domain.  
CC -!- SIMILARITY: Contains 1 J domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M12544; AAA00009.1; -;  
CC EMBL; M12565; AAA23693.1; -;  
CC EMBL; D10483; BAB96590.1; -;  
CC EMBL; U00096; AAC73126.1; -;  
CC PIR; A92572; HHECDJ.  
CC PDB; 1BQ0; NMR; @=1-103.  
CC PDB; 1BQ2; NMR; @=1-77.  
CC PDB; 1EXK; NMR; A=130-208.  
CC PDB; 1XBL; NMR; @=1-107.  
CC ECO2DBASE; H036.5; 6TH EDITION.  
CC EcoGene; EB0236; -;  
CC EcoGene; EG10240; dnaJ.  
CC InterPro; IPR002939; DnaJ\_C.  
CC InterPro; IPR001305; DnaJ\_CXKXGXG.  
CC InterPro; IPR001623; DnaJ\_N.  
CC InterPro; IPR008971; HSP40\_DnaJ\_pap.  
CC InterPro; IPR003095; Hsp\_DnaJ.  
CC InterPro; IPR011031; Multisubunit\_cyt.  
CC Pfam; PF00226; DnaJ; 1.  
CC Pfam; PF01556; DnaJ\_C; 1.  
CC Pfam; PF00684; DnaJ\_CXKXGXG; 1.  
CC PRINTS; PR00625; DnaJPROTEIN.  
CC SMART; SM00271; DnaJ; 1.  
CC PROSITE; PS00636; DnaJ\_1; 1.  
CC PROSITE; PS00076; DnaJ\_2; 1.  
CC PROSITE; PS00637; DnaJ\_CXKXGXG; 1.  
KW 3D-structure; Chapterone; Complete proteome; Direct protein sequencing;  
KW DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
FT INIT MET 0 0  
FT DOMAIN 2 71 J-domain.  
FT DOMAIN 76 113 Gly-rich.  
FT REPEAT 143 150 CXKXGXG motif.  
FT REPEAT 160 167 CXKXGXG motif.  
FT REPEAT 182 189 CXKXGXG motif.  
FT REPEAT 196 203 CXKXGXG motif.  
FT METAL 143 143 Zinc 1.  
FT METAL 146 146 Zinc 1.  
FT METAL 160 160 Zinc 2.  
FT METAL 163 163 Zinc 2.  
FT METAL 182 182 Zinc 2.  
FT METAL 185 185 Zinc 2.  
FT METAL 196 196 Zinc 1.  
FT METAL 199 199 Zinc 1.  
FT HELIX 5 8  
FT TURN 9 10  
FT TURN 13 14  
FT HELIX 18 31  
FT TURN 32 35  
FT HELIX 36 38  
FT TURN 41 42  
FT HELIX 43 50  
FT TURN 51 51  
FT HELIX 52 56  
FT HELIX 59 64  
FT TURN 65 67  
FT TURN 68 73  
FT TURN 131 133  
FT STRAND 140 142

FT HELIX 144 146  
FT TURN 147 149  
FT STRAND 151 151  
FT STRAND 158 159  
FT TURN 161 165  
FT STRAND 168 173  
FT TURN 174 175  
FT STRAND 176 181  
FT TURN 183 187  
FT STRAND 190 191  
FT STRAND 195 195  
FT HELIX 197 199  
FT TURN 200 201  
FT STRAND 204 206  
SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0B8C3F CRC64;  
Query Match 100.0%; Score 81; DB 1; Length 375;  
Best Local Similarity 100.0%; Pred. No. 9.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYGHAAFE 15  
DB 60 OKRAAYDQYGHAAFE 74  
RESULT 3  
ID Q7UDU1 PRELIMINARY; PRT; 376 AA.  
AC Q7UDU1;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Chapterone with DnaJ; heat shock protein.  
GN Names=dnaJ; OrderedLocusNames=S0015;  
OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Shigella.  
OX NCBI\_TaxID=623;  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=2457T;  
RC MEDLINE=22590274; PubMed=12704152;  
RX DOI=10.1128/JAI.71.5.2775-2786.2003;  
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,  
RA Schwartz D.C., Blattner F.R.;  
RT "Complete genome sequence and comparative genomics of Shigella  
RT flexneri serotype 2a strain 2457T.";  
RL Infect. Immun. 71:2775-2786(2003).  
DR EMBL; AS016978; AAP15561.1; -;  
DR HSSP; P08622; 1EXK.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXKXGXG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR Pfam; PF0226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXKXGXG; 1.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXKXGXG; 1.  
KW Heat shock.  
SQ SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;  
Query Match 100.0%; Score 81; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||  
61 QKRAAYDQYGHAAFE 75

# RESULT 4

Q8FLC5 Q8FLC5 PRELIMINARY; PRT; 376 AA.  
AC Q8FLC5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Chapterone protein dnaJ.  
GN Name=dnaJ; OrderedLocusNames=c0020;  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=217992;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;  
RX MEDLINE=22368234; PubMed=12471157; DOI=10.1073/pnas.252529799;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
of uropathogenic Escherichia coli";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)  
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
the ATPase activity of dnaK (By similarity).  
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AB016755; AAN78520.1; -.  
DR PIR; G85481; G85481.  
DR PIR; G90630; G90630.  
DR HSP; P08622; 1EXK.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0008457; P:response to unfolded protein; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001623; DnaJ\_N.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJ\_CXXCXGXG; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS0076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGXG; 1.  
KW Chapterone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||  
61 QKRAAYDQYGHAAFE 75

# RESULT 5

Q8XA65

ID AC Q8XA65 Q8XA65 PRELIMINARY; PRT; 376 AA.  
DT Q8XA65; Q7AHU4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DE Chapterone with DnaK; heat shock protein (DnaJ protein).  
GN Name=dnaJ; OrderedLocusNames=ECs0015, 20015;  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;  
RX MEDLINE=21074935; PubMed=11266551; DOI=10.1038/35054089;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RMD 0509952 / EHEC;  
RX MEDLINE=21156233; PubMed=11256796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
O157:H7 and genomic comparison with a laboratory strain K-12";  
RL DNA Res. 8:11-22(2001).  
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
the ATPase activity of dnaK (By similarity).  
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AB005178; AAG54315.1; -.  
DR PIR; G85481; G85481.  
DR PIR; G90630; G90630.  
DR HSP; P08622; 1EXK.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJ\_CXXCXGXG; 1.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS0076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGXG; 1.  
KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc;  
KW Complete proteome.  
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||  
|||||

Db 61 QKRAAYDQYGHAAFE 75

## RESULT 6

ID\_DNAJ\_HAEDU : STANDARD; PRT; 377 AA.

AC P48208;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN Name=dnaJ; OrderedLocuNames=HD0188;  
 OS Haemophilus ducreyi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=730;  
 RN [1]

## SEQUENCE FROM N.A.

RC STRAIN=35000HP / ATCC 700724;  
 RA Parsons L.M.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]

## SEQUENCE FROM N.A.

RC STRAIN=35000HP / ATCC 700724;  
 RA Munson R.S., Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,  
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;  
 RA "The complete genome sequence of Haemophilus ducreyi."  
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 CC -1- SIMILARITY: Contains 1 CR domain.  
 CC -1- SIMILARITY: Contains 1 J domain.

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EMBL; U25996; AAB67299.1; --

EMBL; AE017151; AAP95181.1; --

HSSP; P08622; IBQZ.

InterPro; IPR002939; DnaJ\_C.

InterPro; IPR001305; DnaJ\_CXXCXGKG.

InterPro; IPR001623; DnaJ\_N.

InterPro; IPR008971; HSP40\_DnaJ\_pdp.

InterPro; IPR003095; Hsp\_DnaJ.

InterPro; IPR011031; Multitnaem\_cyt.

Pfam; PF00226; DnaJ; 1.

Pfam; PF01556; DnaJ\_C; 1.

Pfam; PF01684; DnaJ\_CXXCXGKG; 1.

PRINTS; PS00625; DnaJ\_CXXCXGKG.

PROSITE; PS00636; DnaJ\_1; 1.

PROSITE; PS00076; DnaJ\_2; 1.

PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;

Metal-binding; Repeat; Zinc.

DOMAIN 3 72 J-domain.

DOMAIN 77 108 Gly-rich.

REPEAT 147 154 CXXCXGKG motif.

REPEAT 164 171 CXXCXGKG motif.

REPEAT 186 193 CXXCXGKG motif.

REPEAT 200 207 CXXCXGKG motif.

METAL 147 147 Zinc 1 (By similarity).

METAL 150 150 Zinc 1 (By similarity).

METAL 164 164 Zinc 2 (By similarity).

METAL 167 167 Zinc 2 (By similarity).

METAL 186 186 Zinc 2 (By similarity).

FT METAL 189 189 Zinc 2 (By similarity).  
 FT METAL 200 200 Zinc 1 (By similarity).  
 FT METAL 203 203 Zinc 1 (By similarity).  
 SQ SEQUENCE 377 AA; 41027 MW; 37E9048F81A1A7A9 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAAFE 75

## RESULT 7

ID\_DNAJ\_SALTY STANDARD; PRT; 378 AA.

AC Q60004;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Chaperone protein dnaJ.

GN Name=dnaJ; OrderedLocuNames=STM0013, STY0013, t0013;

OS Salmonella typhimurium, and

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI\_TaxID=602, 601;

RN [1]

SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2;

RA Stephen R.J., Hinton J.C.D.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.";

RL Nature 413:852-856 (2001).

RN [3]

SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

RA Krog A., Larsen T.S., Leather S., Moule S., O'Goara P., Parry C.,

RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrall B.G.;

RA "Complete genome sequence of a multiple drug resistant Salmonella

RT enterica serovar Typhi CT18.";

RL Nature 413:848-852 (2001).

RN [4]

SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;

RX MEDLINE=22531367; PubMed=12644504;

RX DOI=10.1128/JB.185.7.2330-2337.2003;

RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;

RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2

RT and CT18.";

RL J. Bacteriol. 185:2330-2337 (2003).

CC -1- FUNCTION: Interacts with dnaK to disassemble a protein complex at

CC the phage lambda origin of replication. Stimulates, jointly with

CC grpE, the ATPase activity of dnaK.

```
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- INDUCTION: By heat shock under the control of the htpR regulatory
CC protein (By similarity).
CC -|- SIMILARITY: Belongs to the dnaJ family.
CC -|- SIMILARITY: Contains 1 CR domain.
CC -|- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U58360; AAB02911.1; -.
CC EMBL; AB008693; AAL18977.1; -.
CC EMBL; AL627265; CAD01166.1; -.
CC EMBL; AB016834; AAO67747.1; -.
CC HSP; P08622; 1EXX.
CC StyGene; SG10620; dnaJ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGXG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pdp.
CC InterPro; IPR003095; Hsp DnaJ.
CC InterPro; IPR011031; Multihem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGXG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS50076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
CC Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT INIT MET 0 0 By similarity.
FT DOMAIN 2 71 J-domain.
FT REPEAT 76 112 Gly-rich.
FT REPEAT 146 153 CXXCXGXG motif.
FT REPEAT 163 170 CXXCXGXG motif.
FT REPEAT 185 192 CXXCXGXG motif.
FT REPEAT 199 206 CXXCXGXG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 378 AA; 41181 MW; 176EEC64696F30A2 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDQYGHAAFE 74
|||||
RESULT 8
Q8L3D3 PRELIMINARY; PRT; 379 AA.
AC Q8L3D3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 40.
```

```
GN Name=dnaJ;
OS Colwellia maris (Vibrio sp. (strain ABE-11)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Colwelliaceae; Colwellia.
OX NCBI_TaxID=77524;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB084455; BAB91324.2; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; P:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Heat shock.
SQ SEQUENCE 379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75
|||||
RESULT 9
Q66ES9 PRELIMINARY; PRT; 379 AA.
AC Q66ES9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein, DnaJ and GrpE stimulates ATPase activity of
DE DnaK.
GN Name=dnaJ; Synonyms=grpP, grpC; ORFNames=YPTB0612;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G.; Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pseudotuberculosis."
RT genome comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX936398; CAH19852.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
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DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXKXGKXG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR InterPro; IPR011031; Multihnaem\_cyt.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXKXGKXG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXKXGKXG; 1.  
 DR KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
 |||||  
 DB 61 QKRAAYDQYGHAAPE 75

## RESULT 10

ID Q75WD2 PRELIMINARY; PRT; 379 AA.  
 AC Q75WD2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DN DnaJ.  
 GN Name=dnaJ;  
 OS Acetobacter aceti.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Acetobacteraceae; Acetobacter.  
 OX NCBI\_TaxID=435;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IFO3283;  
 RA Okamoto-Kainuma A., Wan Y., Fukaya M., Tsukamoto Y., Ishikawa M.,  
 RA Koizumi Y.;  
 RT "Cloning and Characterization of the dnaJ Operon in Acetobacter  
 aceti.";  
 RL J. Biosci. Bioeng. 97:339-342(2004).  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AB121676; BAD14920.1; -;  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002933; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXKXGKXG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXKXGKXG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ\_1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 379 AA; 41091 MW; CFF54BF1559A75B CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15  
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 DB 62 QKRAAYDQYGHAAPE 76

## RESULT 11

ID Q8ZIM6 PRELIMINARY; PRT; 379 AA.  
 AC Q8ZIM6; Q74Q12; Q7CG76;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Chaperone protein DnaJ (Chaperone with DnaK; heat shock protein).  
 GN Name=dnaJ; Synonyms=dnaJ2, grpP;  
 GN OrderedLocustNames=Yp3711, YP00469, Y3705;  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
 RA Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cardeno-Tarraga A.-M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Feltwell T., Hamlin N., Holtroyd S., Jagsels K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
 RL Nature 413:523-527(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIMS / Biovar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RX DOI=10.1128/JB.184.16.4601-4611.2002;  
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,  
 RA Ferry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM.";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=91001 / Biovar Mediaevalis;  
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,  
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,  
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,  
 RA Yang R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AJ414142; CAC89325.1; -;  
 DR EMBL; AE013974; AAM87253.1; -;  
 DR EMBL; AB017141; AAS63859.1; -;  
 DR FIr; AB0058; AB0058.  
 DR HSSP; P08622; 1EXK.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXKXGKXG; 1.

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DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 13
DnaJ_HAEIN
ID_DNAJ_HAEIN STANDARD; PRT; 382 AA.
AC P43735;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=H11238;
OS Haemophilus influenzae;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D.; Adams M.D.; White O.; Clayton R.A.; Kirkness E.F.;
RA Klenzwe A.R.; Bult C.J.; Tomb J.-F.; Dougherty B.A.; Merrick J.M.;
RA McKelvey K.; Sutton G.G.; FitzHugh W.; Fields C.A.; Gocayne J.D.;
RA Scott J.D.; Shirley R.; Liu L.-I.; Glodek A.; Kelley J.M.;
RA Weidman J.F.; Phillips C.A.; Spriggs T.; Hedblom E.; Cotton M.D.;
RA Utterback T.R.; Hanna M.C.; Nguyen D.T.; Saudek D.M.; Brandon R.C.;
RA Fine L.D.; Fritchman J.L.; Fuhrmann J.L.; Geoghagen N.S.M.;
RA Gnehm C.L.; McDonald L.A.; Small K.V.; Fraser C.M.; Smith H.O.;
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RT Science 269:496-512 (1995).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; U32803; AAC22890.1; ALT_INIT.
DR HSP; P08622; 1BQZ.
DR TIGR; H11238; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
KW

RESULT 12
Q6D0B8
ID Q6D0B8 PRELIMINARY; PRT; 379 AA.
AC Q6D0B8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone protein DnaJ.
GN Name=dnaJ; OrderedLocusNames=ECA3881;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S.; Sebaihia M.; Pritchard L.; Holden M.T.G.; Hyman L.J.;
RA Holeva M.C.; Thomson N.R.; Bentley S.D.; Churcher L.J.C.; Mungall K.;
RA Atkin R.; Bason N.; Brooks K.; Chillingworth T.; Clark K.; Doggett J.;
RA Fraser A.; Hance Z.; Hauser H.; Jagels K.; Moule S.; Norbertczak H.;
RA Ormond D.; Price C.; Quail M.A.; Sanders M.; Walker D.; Whitehead S.;
RA Salmond G.P.C.; Birch P.R.J.; Parkhill J.; Toth I.K.;
RA "Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC EMBL; BX950851; CAG76779.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
KW
SQ SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;
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FT DOMAIN 3 72 J-domain.
FT DOMAIN 77 110 GLY-rich.
FT REPEAT 147 154 CXKXGKG motif.
FT REPEAT 164 171 CXKXGKG motif.
FT REPEAT 186 193 CXKXGKG motif.
FT REPEAT 200 207 CXKXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 382 AA; 41222 MW; 88508886FB2BC2B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QKRAAYDQYGHAAFE 15
Db 61 QKRAAYDQYGHAAFE 75

RESULT 14
O83MH4 PRELIMINARY; PRT; 386 AA.
AC O83MH4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chapterone with DnaK; heat shock protein.
GN Name=dnaJ; OrderedLocusNames=SF0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC ENBL; AE015039; AAN41681.1; -.
DR HSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:006260; P:DNA replication; IEA.
DR GO; GO:006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00684; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00637; DnaJ_2; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT DOMAIN 77 110 Gly-rich.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_2; 1.
DR Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;

Query Match 100.0%; Score 81; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QKRAAYDQYGHAAFE 15
Db 71 QKRAAYDQYGHAAFE 85

RESULT 15
DnaJ ACTAC
ID DnaJ ACTAC STANDARD; PRT; 375 AA.
AC P77856;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ;
OS Actinobacillus actinomycetemcomitans (Haemophilus
OC actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y4;
RX MEDLINE=98182595; PubMed=9522128;
RA Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.;
RT "Isolation and characterization of the dnaK operon from
RT Actinobacillus actinomycetemcomitans."
RL DNA Seq. 8:93-98(1997).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; D87753; BAA32697.1; -.
DR HSP; P08622; 1BOZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00637; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT DOMAIN 77 110 Gly-rich.
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```
FT REPEAT      145      152      CXXCXGXG motif.
FT REPEAT      162      169      CXXCXGXG motif.
FT REPEAT      184      191      CXXCXGXG motif.
FT REPEAT      198      205      CXXCXGXG motif.
FT METAL       145      145      Zinc 1 (By similarity).
FT METAL       148      148      Zinc 1 (By similarity).
FT METAL       162      162      Zinc 2 (By similarity).
FT METAL       165      165      Zinc 2 (By similarity).
FT METAL       184      184      Zinc 2 (By similarity).
FT METAL       187      187      Zinc 2 (By similarity).
FT METAL       198      198      Zinc 1 (By similarity).
FT METAL       201      201      Zinc 1 (By similarity).
SQ SEQUENCE    375 AA; 41374 MW; CFS9D286756FF44E1 CRC64;
Query Match      96.3%; Score 78; DB 1; Length 375;
Best Local Similarity 93.3%; Pred. No. 3.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15
DB 61 EKRAAYDQYGHAAPE 75

RESULT 16
ID Q6LUAG PRELIMINARY; PRT; 380 AA.
AC O6LUAG;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative DnaJ protein, DnaJ-class molecular chaperone with C-terminal
DE Zn finger domain.
GN Name=EC50015; OrderedLocusNames=PPRA0698;
OS Bacterium; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN SEQUENCE FROM N.A.
RP Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; CR378665; CAG19119.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40 DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF02266; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ 1; 1.
DR PROSITE; PS0076; DnaJ 2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
SQ SEQUENCE    380 AA; 40802 MW; 772DD9F069899B63 CRC64;
Query Match      96.3%; Score 78; DB 2; Length 380;
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Best Local Similarity 93.3%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAPE 15
DB 60 QKRAAYDQYGHAAPE 74

RESULT 17
ID Dnaj_VIBCH STANDARD; PRT; 381 AA.
AC O34242; O9KTP5;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=VC0856;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN SEQUENCE FROM N.A.
RP STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN SEQUENCE OF 1-80 FROM N.A.
RP STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
RX MEDLINE=99150229; PubMed=10024539;
RA Chakrabarti S., Sengupta N., Chowdhury R.;
RT "Role of DnaK in vitro and in vivo expression of virulence factors
RT of Vibrio cholerae.";
RL Infect. Immun. 67:1025-1033(1999).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AE004171; AAF94018.1; -.
DR EMBL; Y14237; CAA74628.1; -.
DR PIR; D82270; D82270.
DR HSP; P08622; 1BQZ.
DR TIGR; VC0856; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40 DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multisubunit.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
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DR PRINTS; PR00625; DnaJ C.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ; 1; 1.  
DR PROSITE; PS00076; DnaJ; 2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
FT DOMAIN 4 72  
FT J-domain.  
FT REPEAT 77 119  
FT Gly-rich.  
FT REPEAT 149 156  
FT CXXCXGKG motif.  
FT REPEAT 166 173  
FT CXXCXGKG motif.  
FT REPEAT 188 195  
FT CXXCXGKG motif.  
FT REPEAT 202 209  
FT CXXCXGKG motif.  
FT METAL 149 149  
FT Zinc 1 (By similarity).  
FT METAL 152 152  
FT Zinc 1 (By similarity).  
FT METAL 166 166  
FT Zinc 2 (By similarity).  
FT METAL 169 169  
FT Zinc 2 (By similarity).  
FT METAL 188 188  
FT Zinc 2 (By similarity).  
FT METAL 191 191  
FT Zinc 1 (By similarity).  
FT METAL 202 202  
FT Zinc 1 (By similarity).  
FT METAL 205 205  
FT Zinc 1 (By similarity).  
FT METAL 205 205  
FT Zinc 1 (By similarity).  
FT CONFLICT 37 38  
FT NS -> TP (in Ref. 2).  
FT CONFLICT 43 45  
FT AAE -> CRG (in Ref. 2).  
FT CONFLICT 49 51  
FT EVK -> IQ (in Ref. 2).  
FT CONFLICT 67 67  
FT D -> E (in Ref. 2).  
FT CONFLICT 71 71  
FT H -> I (in Ref. 2).  
FT CONFLICT 78 80  
FT AGG -> RVV (in Ref. 2).  
SQ SEQUENCE 381 AA; 40822 MW; 2188BE36D0315D5 CRC64;

Query Match 96.3%; Score 78; DB 1; Length 381;  
Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKKAAYDQYGHAAFE 15  
Db 61 QKKAAYDQYGHAAFE 75  
||:|||||

## RESULT 18

Q87RX2 PRELIMINARY; PRT; 381 AA.  
AC Q87RX2; TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein.  
GN OrderedLocusNames=VP0654;  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RMD.2210633 / Serotype O3:K6;  
RA MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
RX Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";  
RL Lancet 361:743-749(2003).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL; AP005075; BAC58917.1; -.  
DR HSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
Q87RX2 PRELIMINARY; PRT; 381 AA.  
AC Q87RX2; TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein.  
GN OrderedLocusNames=VP0654;  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RMD.2210633 / Serotype O3:K6;  
RA MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
RX Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";  
RL Lancet 361:743-749(2003).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL; AP005075; BAC58917.1; -.  
DR HSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.

DR InterPro; IPR002939; DnaJ C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJ C.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ 1; 1.  
DR PROSITE; PS00076; DnaJ 2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 381 AA; 41026 MW; F1DC4DCB64ACD4C6 CRC64;

Query Match 96.3%; Score 78; DB 2; Length 381;  
Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKKAAYDQYGHAAFE 15  
Db 61 QKKAAYDQYGHAAFE 75  
||:|||||

## RESULT 19

Q8DF67 PRELIMINARY; PRT; 381 AA.  
AC Q8DF67; TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ chaperone.  
GN OrderedLocusNames=VV10354;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AS016798; AAC08881.1; -.  
DR HSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJ C.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ 1; 1.  
DR PROSITE; PS00076; DnaJ 2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 381 AA; 41226 MW; 1F0783454AE538A6 CRC64;

Query Match 96.3%; Score 78; DB 2; Length 381;  
 Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
 ||:|||||  
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 20  
 ID DNAJ\_VIBHA STANDARD; PRT; 385 AA.  
 AC O87385;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN Name=dnaJ;  
 OS Vibrio harveyi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=669;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98418481; PubMed=9747709; DOI=10.1007/s004380050803;  
 RA Klein G., Zmijewski M., Krzewska J., Czeckatka M., Lipinska B.,  
 RT "Cloning and characterization of the dnaK heat shock operon of the  
 marine bacterium Vibrio harveyi.";  
 RL Mol. Gen. Genet. 259:179-189 (1998).  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grps,  
 the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 CC -!- SIMILARITY: Contains 1 CR domain.  
 CC -!- SIMILARITY: Contains 1 J domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AY639008; AAT39537.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp DnaJ.  
 DR InterPro; IPR011031; Multihaem\_cyt.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 FT DOMAIN 5 70 U-domain.  
 FT DOMAIN 77 120 Gly-rich.  
 FT REPEAT 150 157 CXXCXGKG motif.  
 FT REPEAT 167 174 CXXCXGKG motif.  
 FT REPEAT 189 196 CXXCXGKG motif.  
 FT REPEAT 202 209 CXXCXGKG motif.  
 FT METAL 150 150 Zinc 1 (By similarity).

FT METAL 153 153 Zinc 1 (By similarity).  
 FT METAL 167 167 Zinc 2 (By similarity).  
 FT METAL 170 170 Zinc 2 (By similarity).  
 FT METAL 189 189 Zinc 2 (By similarity).  
 FT METAL 192 192 Zinc 2 (By similarity).  
 FT METAL 202 202 Zinc 1 (By similarity).  
 FT METAL 205 205 Zinc 1 (By similarity).  
 SQ SEQUENCE 385 AA; 41619 MW; ABA1BS2321D15F58 CRC64;

Query Match 96.3%; Score 78; DB 1; Length 385;  
 Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15  
 ||:|||||  
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 21  
 ID Q7MN84 PRELIMINARY; PRT; 386 AA.  
 AC Q7MN84;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN OrderedLocusNames=V08833;  
 OS Vibrio vulnificus (strain VJ016).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=196600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14656965; DOI=10.1101/gr.1295503;  
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
 RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen H.-T., Li J.-C., Su T.-L.,  
 RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.,  
 RT "Comparative genome analysis of Vibrio vulnificus, a marine  
 pathogen.";  
 RL Genome Res. 13:2577-2587(2003).  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grps,  
 the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 DR EMBL; AP005333; BAC93597.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006240; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp DnaJ.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 386 AA; 41786 MW; A774299EF281D6C0 CRC64;

Query Match 96.3%; Score 78; DB 2; Length 386;  
 Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 66 OKRAAYDOYGHAAFE 80

## RESULT 22

ID Q65U54 PRELIMINARY; PRT; 389 AA.  
AC Q65U54;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE DnaJ protein.  
GN Name=dnaJ; ORFNames=MS0899;  
OS Mannheimia succiniciproducens MBEL55E.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Mannheimia.  
OX NCBI\_TaxID=221988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MBEL55E;  
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;  
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia  
succiniciproducens";  
RL Nat. Biotechnol. 0:0-0(2004).  
DR EMBL; AE016827; AAU37506.1; -.  
SQ SEQUENCE 389 AA; 42555 MW; 8DE1A0A8A47374B CRC64;

Query Match 96.3%; Score 78; DB 2; Length 389;  
Best Local Similarity 93.3%; Pred. No. 3.4e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 74 EKRAAYDOYGHAAFE 88

## RESULT 23

ID DNAJ\_RHILE STANDARD; PRT; 234 AA.  
AC O33529;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Chaperone protein dnaJ (Fragment).  
GN Name=dnaJ, leguminosarum.  
OS Rhizobium leguminosarum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=384;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=8401:PRLI;  
RA Simpkins S.A., Johnston A.W.B., James R.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the dnaJ family.  
CC -1- SIMILARITY: Contains 1 CR domain.  
CC -1- SIMILARITY: Contains 1 J domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Y14649; CAA74983.1; -.

DR HSP; P08622; 1BQZ.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM0271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
FT DOMAIN 3 72 J-domain.  
FT DOMAIN 77 119 Gly-rich.  
FT REPEAT 149 156 CXXCXGKG motif.  
FT REPEAT 166 173 CXXCXGKG motif.  
FT REPEAT 188 195 CXXCXGKG motif.  
FT REPEAT 202 209 CXXCXGKG motif.  
FT METAL 149 149 Zinc 1 (By similarity).  
FT METAL 152 152 Zinc 1 (By similarity).  
FT METAL 166 166 Zinc 2 (By similarity).  
FT METAL 169 169 Zinc 2 (By similarity).  
FT METAL 188 188 Zinc 2 (By similarity).  
FT METAL 191 191 Zinc 2 (By similarity).  
FT METAL 202 202 Zinc 1 (By similarity).  
FT METAL 205 205 Zinc 1 (By similarity).  
FT NON\_TER 234 234.  
SQ SEQUENCE 234 AA; 25268 MW; 2D8361F8495164E3 CRC64;

Query Match 95.1%; Score 77; DB 1; Length 234;  
Best Local Similarity 93.3%; Pred. No. 3.1e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYGHAAFE 15  
Db 61 OKRAAYDOYGHAAFE 75

## RESULT 24

ID Q93S23 PRELIMINARY; PRT; 331 AA.  
AC Q93S23;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein (Fragment).  
GN Name=dnaJ;  
OS Rhizobium tropici.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=398;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CIAT899;  
RA Sanjuan J.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the dnaJ family.  
CC EMBL; AJ311186; CAC38775.1; -.  
DR HSP; P08622; 1BQZ.  
DR GO; GO:0051082; P:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.

DR	InterPro; IPR003095; Hsp_DnaJ.
DR	Pfam; PF00226; DnaJ_1.
DR	Pfam; PF01556; DnaJ_C; 1.
DR	Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR	PRINTS; PR00625; DNAJPROTEIN.
DR	SMART; SM00271; DnaJ; 1.
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR	PROSITE; PS00636; DnaJ_1; 1.
DR	PROSITE; PS00076; DnaJ_2; 1.
DR	PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR	Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW	NON_TER 1
FT	NON_TER 331 331
FT	SEQUENCE 331 AA; 35577 MW; B2566D48E002A2C5 CRC64;
SQ	
Query Match 95.1%; Score 77; DB 2; Length 331; Best Local Similarity 93.3%; Pred. No. 4.e-05; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 OKRAAYDOYGHAAFE 15      :
Db	39 QKRAYDRYGHAAFE 53      :
RESULT 25	
ID	Q92T07 PRELIMINARY; PRT; 379 AA.
AC	Q92T07
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	PROBABLE CHAPERONE PROTEIN.
GN	OFAName-SMc02858;
OS	Rhizobium meliloti (Sinorhizobium meliloti).
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;	
CC	[1]
CC	SEQUENCE FROM N.A.
RP	STRAIN=1021.
RX	MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA	Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA	Boisard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA	Godrie T., Goffeau A., Kahn D., Kiss E., Lelauré V., Masuy D.,
RA	Pohl T., Portetelle D., Puhler A., Purnelle B., Rameperger U.,
RA	Renard C., Thebaud P., Vandenberg M., Weidner S., Galibert F.;
RA	"Analysis of the chromosome sequence of the legume symbiont
RT	Sinorhizobium meliloti strain 1021";
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC	-1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC	the ATPase activity of dnaK (By similarity).
CC	-1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-1- SIMILARITY: Belongs to the dnaJ family.
DR	EMBL; AL591782; CAC41570.1; -.
DR	HSP; P08622; IBOZ.
DR	GO; GO:0051082; F:unfolded protein binding; IEA.
DR	GO; GO:0006260; P:DNA replication; IEA.
DR	GO; GO:0006457; P:protein folding; IEA.
DR	GO; GO:0006986; P:response to unfolded protein; IEA.
DR	InterPro; IPR000345; CytC_heme_BS.
DR	InterPro; IPR002933; DnaJ_C.
DR	InterPro; IPR001305; DnaJ_N.
DR	InterPro; IPR001623; DnaJ_N.
DR	InterPro; IPR008971; HSP40_DnaJ_pdp.
DR	InterPro; IPR003095; Hsp_DnaJ.
DR	Pfam; PF00226; DnaJ; 1.
DR	Pfam; PF01556; DnaJ_C; 1.
DR	Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR	PRINTS; PR00625; DNAJPROTEIN.
DR	SMART; SM00271; DnaJ; 1.
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR	PROSITE; PS00636; DnaJ_1; 1.
DR	PROSITE; PS00076; DnaJ_2; 1.
DR	Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW	NON_TER 1
FT	NON_TER 331 331
FT	SEQUENCE 331 AA; 35577 MW; B2566D48E002A2C5 CRC64;
SQ	
Query Match 95.1%; Score 77; DB 2; Length 331; Best Local Similarity 93.3%; Pred. No. 4.e-05; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 OKRAAYDOYGHAAFE 15      :
Db	39 QKRAYDRYGHAAFE 53      :
RESULT 26	
ID	NOLC_RHIFR STANDARD; PRT; 392 AA.
AC	P26508;
DT	01-AUG-1992 (Rel. 23, Created)
DT	01-AUG-1992 (Rel. 23, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	NolC protein.
GN	Name=nolC;
OS	Rhizobium fredii (Sinorhizobium fredii).
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=380;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=USDA 257;
RX	MEDLINE=G1260457; PubMed=1646377;
RA	Krishnan H.B., Pueppke S.G.;
RA	"nolC, a Rhizobium fredii gene involved in cultivar-specific
RT	nodulation of soybean, shares homology with a heat-shock gene.";
RL	Mol. Microbiol. 5:737-745(1991).
CC	-1- SIMILARITY: Contains 1 J domain.
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L03521; AAA26333.1; -.
DR	PIR; S15295; S15295.
DR	HSP; P08622; IBOZ.
DR	InterPro; IPR002939; DnaJ_C.
DR	InterPro; IPR001623; DnaJ_N.
DR	InterPro; IPR008971; HSP40_DnaJ_pdp.
DR	InterPro; IPR003095; Hsp_DnaJ.
DR	Pfam; PF00226; DnaJ; 1.
DR	Pfam; PF01556; DnaJ_C; 1.
DR	PRINTS; PR00625; DNAJPROTEIN.
DR	SMART; SM00271; DnaJ; 1.
DR	PROSITE; PS00636; DnaJ_1; 1.
DR	PROSITE; PS00076; DnaJ_2; 1.
KW	Chaperone; Nodulation.
FT	DOMAIN 2 71 J-domain.
FT	DOMAIN 76 93 Gly-rich.
FT	DOMAIN 96 121 Arg-rich.
SQ	SEQUENCE 392 AA; 43565 MW; B60F6DB27980F324 CRC64;
Query Match 95.1%; Score 77; DB 1; Length 392; Best Local Similarity 93.3%; Pred. No. 5.2e-05; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 OKRAAYDOYGHAAFE 15      :
Db	60 QKRAYDRYGHAAFE 74      :

```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
Db 61 OKRAAYDQYGHAAFE 75

RESULT 28
DNAJ_BUCAI
ID _DNAJ_BUCAI STANDARD; PRT; 377 AA.
AC O32465;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=PM0740;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Enterobacteriaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Pautian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE006111; BAK02824.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_CXXCXGKG.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40_DnaJ_pap.
CC InterPro: IPR003095; Hsp_DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC PRINTS; P00684; DnaJ_CXXCXGKG; 1.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; FALSE NEG.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.

QY 1 OKRAAYDQYGHAAFE 15
Db 61 OKRAAYDQYGHAAFE 75

RESULT 27
DNAJ_PASMU
ID _DNAJ_PASMU STANDARD; PRT; 372 AA.
AC Q9CNS2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=PM0740;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Enterobacteriaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Pautian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE006111; BAK02824.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_CXXCXGKG.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40_DnaJ_pap.
CC InterPro: IPR003095; Hsp_DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ_C; 1.
CC PRINTS; P00684; DnaJ_CXXCXGKG; 1.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 143 150 Gly-rich.
FT REPEAT 160 167 CXXCXGKG motif.
FT REPEAT 182 189 CXXCXGKG motif.
FT REPEAT 196 203 CXXCXGKG motif.
FT METAL 143 143 Zinc 1 (By similarity).
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 160 160 Zinc 2 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 182 182 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
SQ SEQUENCE 372 AA; 40776 MW; 339B5FE137211D9A CRC64;

Query Match 92.6%; Score 75; DB 1; Length 372;
Best Local Similarity 93.3%; Pred. No. 0.00011;

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Pfam: PF00684; DnaJ\_CXXCXGXG; 1.

DR PRINTS: PR00625; DNAJPROTEIN.  
DR SMART: SM00271; DnaJ\_1.  
DR PROSITE: PS00636; DNAJ\_1; 1.  
DR PROSITE: PS00637; DNAJ\_CXXCXGXG; FALSE NEG.  
KW Chapterone: Complete proteome; DNA replication; Heat shock;  
Metal-binding; Repeat; Zinc. J-domain.  
FT DOMAIN 77 116 Gly-rich.  
FT REPEAT 146 153 CXXCXGXG motif.  
FT REPEAT 163 170 CXXCXGXG motif.  
FT REPEAT 185 192 CXXCXGXG motif.  
FT REPEAT 199 206 CXXCXGXG motif.  
FT METAL 146 146 Zinc 1 (By similarity).  
FT METAL 149 149 Zinc 1 (By similarity).  
FT METAL 163 163 Zinc 2 (By similarity).  
FT METAL 166 166 Zinc 2 (By similarity).  
FT METAL 185 185 Zinc 2 (By similarity).  
FT METAL 188 188 Zinc 2 (By similarity).  
FT METAL 199 199 Zinc 1 (By similarity).  
FT METAL 202 202 Zinc 1 (By similarity).  
SQ SEQUENCE 378 AA; 42469 MW; BB73F48DAF7A2B34 CRC64;

Query Match 91.4%; Score 74; DB 1; Length 378;  
Best Local Similarity 86.7%; Pred. No. 0.00017;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QKRAAYDQYGHAAFE 15  
Db 61 EKRTAYDQYGHAAFE 75

RESULT 30

DNAJ\_NEIMA STANDARD; PRT; 373 AA.

ID DNAJ\_NEIMA STANDARD; PRT; 373 AA.  
AC P63968; PS7107;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Chaperone protein dnaJ  
GN Name=dnaJ; OrderedLocNames=NMA0209;  
OS Neisseria meningitidis (serogroup A).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=Z2491 / Serogroup A / Serotype 4A;  
RX STRAINS=2022556; PubMed=10761919; DOI=10.1038/35006655;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,  
RA Klee S.R., Morelli G., Baoham D., Brown D., Chillingworth T.,  
RA Davies R.M., Davis P., Devlin K., Feltwell K.L., Quail M.A.,  
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,  
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
RA Whitehead S., Spratt B.G., Barrell B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491".  
RL Nature 404:502-506(2000).  
CC - FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
the ATPase activity of dnaK (By similarity).  
CC - COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC - SIMILARITY: Belongs to the dnaJ family.  
CC - SIMILARITY: Contains 1 CR domain.  
CC - SIMILARITY: Contains 1 J domain.  
-----  
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or send an email to license@isb-sib.ch).

EMBL; AE014090; AAM67713.1; -.  
HSP; P08622; 1BQZ.  
DR InterPro: IPR002939; DnaJ\_C.  
DR InterPro: IPR001305; DnaJ\_CXXCXGXG.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR008971; HSP40\_DnaJ\_pgp.  
DR InterPro: IPR003095; Hsp\_DnaJ.  
DR InterPro: IPR011031; Multihaem\_cyt.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.

```

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CC EMBL; AL162752; CAB83522.1; -.
CC HSSP; P08622; 1BQZ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; Hsp40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 147 154 Gly-rich.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 186 193 CXXCXGKG motif.
FT REPEAT 200 207 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 373 AA; 40585 MW; 4D881E20A5D831CF CRC64;

Query Match 90.1%; Score 73; DB 1; Length 373;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db :|||||
61 EKRAAYDQYGHAAFE 75

RESULT 31
DnaJ_NEIMB STANDARD; PRT; 373 AA.
AC P63969; P57107;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=NMB0059;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hackney E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittiore H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";

```

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Science 287:1809-1815(2000).
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
-!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Contains 1 CR domain.
-!- SIMILARITY: Contains 1 J domain.
-----
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-----
CC EMBL; AS002365; AAP40528.1; -.
CC PIR; D81242; D81242.
CC HSSP; P08622; 1BQZ.
CC TIGR; NMB0059; -.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; Hsp40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT REPEAT 147 154 Gly-rich.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 186 193 CXXCXGKG motif.
FT REPEAT 200 207 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 373 AA; 40585 MW; 4D881E20A5D831CF CRC64;

Query Match 90.1%; Score 73; DB 1; Length 373;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db :|||||
61 EKRAAYDQYGHAAFE 75

RESULT 32
DnaJ_BRUOV STANDARD; PRT; 375 AA.
AC Q05980;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
DE Name=dnaJ;
OS Brucella ovis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

```

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OC Brucellaceae; Brucella.
OX NCBI_TaxID=236;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 25840 / 63/290T;
RE MEDLINE=93094135; PubMed=1459952;
RA Cellier M.F.M., Teyssier J., Nicolas M., Liautard J.P., Marti J.,
RT "Cloning and characterization of the Brucella ovis heat shock protein
RT DnaK functionally expressed in Escherichia coli.";
RL J. Bacteriol. 174:8036-8042(1992).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
DR EMBL; M95799; AAC36133.1; -.
DR PIR; B47042; B47042.
DR HSP; P08622; 1BQ2.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_p.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00706; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT DOMAIN 77 106 Gly-rich.
FT REPEAT 146 133 CXXCXGKG motif.
FT REPEAT 163 170 CXXCXGKG motif.
FT REPEAT 185 192 CXXCXGKG motif.
FT REPEAT 199 206 CXXCXGKG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 2 (By similarity).
FT METAL 163 163 Zinc 1 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 1 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 375 AA; 41021 MW; 61CB5F99FA2DC73D CRC64;

Query Match 90.1%; Score 73; DB 1; Length 375;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 33
Q98DD2
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ID Q98DD2 PRELIMINARY; PRT; 376 AA.
AC Q98DD2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein; DnaJ.
GN OrderedLocuNames=ml14755;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuoto M., Matsuono A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AP003004; BAB51339.1; -.
DR HSP; P08622; 1BQ2.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006250; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_p.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00706; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 376 AA; 41201 MW; AFA2EAB4C2186E7 CRC64;

Query Match 90.1%; Score 73; DB 2; Length 376;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 34
DnaJ_AGR75
ID DnaJ_AGR75 STANDARD; PRT; 377 AA.
AC P50018;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocuNames=Atu0121, AGR_C_192;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
```



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OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RL C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaubin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
RN [3]
RP SEQUENCE OF 1-66 FROM N.A.
RX MEDLINE=96011387; PubMed=7592349;
RA Segal G., Ron E.Z.;
RT "The dnaJ operon of Agrobacterium tumefaciens: transcriptional
RT analysis and evidence for a new heat shock promoter."
RL J. Bacteriol. 177:5952-5958 (1995).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; AE008986; AAU41146.1; -.
CC DR EMBL; AE007953; AAX85941.1; -.
CC DR EMBL; X87113; CAA60593.1; -.
CC DR PIR; AD2591; AD2591.
CC DR PIR; D97373; D97373.
CC DR PIR; I39586; I39586.
CC DR HSSP; P08622; 1BQZ.
CC DR InterPro; IPR002939; DnaJ_C.
CC DR InterPro; IPR001305; DnaJ_CXXCXGKG.
CC DR InterPro; IPR001623; DnaJ_N.
CC DR InterPro; IPR003095; Hsp_DnaJ.
CC DR InterPro; IPR001031; Multithaen_cyt.
CC DR Pfam; PF00226; DnaJ_1.
CC DR Pfam; PF01556; DnaJ_C_1.
CC DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC DR PRINTS; PR00625; DnaJPROTEIN.
CC DR SMART; SM00271; DnaJ; 1.
CC DR PROSITE; PS00636; DnaJ_1; 1.
CC DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT DOMAIN 77 109 Gly-rich.
FT REPEAT 151 158 CXXCXGKG motif.
FT REPEAT 168 175 CXXCXGKG motif.
FT REPEAT 190 197 CXXCXGKG motif.
FT REPEAT 204 211 CXXCXGKG motif.
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 171 171 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 193 193 Zinc 2 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
FT METAL 207 207 Zinc 1 (By similarity).
FT CONFLICT 4 4 A -> R (in Ref. 3).
SQ SEQUENCE 377 AA; 40894 MW; 0B6A1D30754D18A CRC64;
Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QKEAAYDQYGHAAFE 15
| | | | | : | | | |
Db 61 QKEAAYDRFGHAAFE 75
RESULT 35
DnaJ BRUME
ID DnaJ BRUME STANDARD; PRT; 377 AA.
AC Q8VE77;
DT 23-MAR-2004 (Rel. 43, Created)
DT 23-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
OS Name=dnaJ; OrderedLocustNames=BMEI2001;
GN Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=294599;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapral V., Redkar R.J., Petra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; AE009632; AAL53182.1; -.
CC DR PIR; AC3502; AC3502.
CC DR HSSP; P08622; 1BQZ.

```

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DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00076; DnaJ_1; 1.
DR PROSITE; PS00636; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT REPEAT 77 106 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 2 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F16606E775 CRC64;

Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDFGHAAFE 74

RESULT 36
DnaJ BRUSU STANDARD; PRT; 377 AA.
AC Q8FXL1;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocustNames=BR2126;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122; DOI=10.1073/pnas.122319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.B., Hoover D.B., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
```

```
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CC -----
CC EMBL; AE014500; AA031016.1; -.
CC PIR; AC3502; AC3502.
CC HSSP; P08622; 1BQZ.
CC TIGR; BR2126; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 4 69 J-domain.
FT REPEAT 77 106 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F16606E775 CRC64;

Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.00025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDFGHAAFE 74

RESULT 37
Q6RSNS PRELIMINARY; PRT; 379 AA.
AC Q6RSNS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DnaJ.
GN Name=dnaJ;
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RUOR.
RA Hennessy F., Boshoff A., Blatch G.L.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL: AY494599; AAR84666.1; -.  
DR GO: GO:0051082; P:unfolded protein binding; IEA.  
DR GO: GO:006260; P:DNA replication; IEA.  
DR GO: GO:0006457; P:protein folding; IEA.  
DR GO: GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro: IPR000345; CytC heme\_BS.  
DR InterPro: IPR002939; DnaJ\_C.  
DR InterPro: IPR001305; DnaJ\_N.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR008971; HSP40 DnaJ\_pap.  
DR Pfam: PF00226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C.  
DR Pfam: PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS: PR00625; DnaJ\_CXXCXGKG; 1.  
DR SMART: SM00271; DnaJ\_C.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00636; DnaJ\_1; 1.  
DR PROSITE: PS00076; DnaJ\_2; 1.  
DR PROSITE: PS00637; DnaJ\_CXXCXGKG; 1.  
DR InterPro: IPR001305; DnaJ\_N.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR008971; HSP40 DnaJ\_pap.  
DR Pfam: PF00226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C.  
DR Pfam: PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS: PR00625; DnaJ\_CXXCXGKG; 1.  
DR SMART: SM00271; DnaJ\_C.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00636; DnaJ\_1; 1.  
DR PROSITE: PS00076; DnaJ\_2; 1.  
DR PROSITE: PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 379 AA; 41069 MW; 42A1B0B3AD41CAD CRC64;  
  
Query Match 90.1%; Score 73; DB 2; Length 379;  
Best Local Similarity 86.7%; Pred. No. 0.00025;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QKRAAYDQYGHAAFE 15  
| | | | | : | | | | |  
Db 61 QKRAAYDRFGHAAFE 75  
  
RESULT 38  
Q6G1F8 PRELIMINARY; PRT; 380 AA.  
AC Q6G1F8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Heat shock protein DnaJ.  
GN Name=dnaJ; OrderedLocustNames=BQ00600;  
OS Bartonella quintana (Rochalimaea quintana).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bartonellaceae; Bartonella.  
OX NCBI\_TaxID=803;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Toulouse;  
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;  
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,  
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,  
RA La Scola B., Holmberg M., Andersson S.G.E.;  
RT "The house-borne human pathogen Bartonella quintana is a genomic  
derivative of the zoonotic agent Bartonella henselae."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL: BX897700; CAP25567.1; -.  
DR GO: GO:0051082; P:unfolded protein binding; IEA.  
DR GO: GO:006260; P:DNA replication; IEA.  
DR GO: GO:0006457; P:protein folding; IEA.  
DR GO: GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro: IPR000345; CytC heme\_BS.  
DR InterPro: IPR002939; DnaJ\_C.  
DR InterPro: IPR001305; DnaJ\_N.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR008971; HSP40 DnaJ\_pap.  
DR Pfam: PF00226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C.  
DR Pfam: PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS: PR00625; DnaJ\_CXXCXGKG; 1.  
DR SMART: SM00271; DnaJ\_C.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00636; DnaJ\_1; 1.  
DR PROSITE: PS00076; DnaJ\_2; 1.  
DR PROSITE: PS00637; DnaJ\_CXXCXGKG; 1.

DR InterPro: IPR005829; Sug\_transporter.  
DR Pfam: PF00226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C.  
DR Pfam: PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS: PR00625; DnaJ\_CXXCXGKG; 1.  
DR SMART: SM00271; DnaJ\_1.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00636; DnaJ\_1; 1.  
DR PROSITE: PS00076; DnaJ\_2; 1.  
DR PROSITE: PS00637; DnaJ\_CXXCXGKG; 1.  
DR PROSITE: PS00217; SUGAR\_TRANSPORT\_2; UNKNOWN\_1.  
DR PROSITE: PS00217; SUGAR\_TRANSPORT\_2; UNKNOWN\_1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 380 AA; 42171 MW; 5B222DB2C5PE0BA8 CRC64;  
  
Query Match 90.1%; Score 73; DB 2; Length 380;  
Best Local Similarity 86.7%; Pred. No. 0.00025;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QKRAAYDQYGHAAFE 15  
| | | | | : | | | | |  
Db 60 QKRAAYDRFGHAAFE 74  
  
RESULT 39  
Q6G553 PRELIMINARY; PRT; 381 AA.  
AC Q6G553;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Heat shock protein DnaJ.  
GN Name=dnaJ1; OrderedLocustNames=BH00660;  
OS Bartonella henselae (Rochalimaea henselae).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bartonellaceae; Bartonella.  
OX NCBI\_TaxID=38323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49882 / Houston 1;  
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;  
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,  
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,  
RA La Scola B., Holmberg M., Andersson S.G.E.;  
RT "The house-borne human pathogen Bartonella quintana is a genomic  
derivative of the zoonotic agent Bartonella henselae."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL: BX897699; CAP26882.1; -.  
DR GO: GO:0051082; P:unfolded protein binding; IEA.  
DR GO: GO:006260; P:DNA replication; IEA.  
DR GO: GO:0006457; P:protein folding; IEA.  
DR GO: GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro: IPR000345; CytC heme\_BS.  
DR InterPro: IPR002939; DnaJ\_C.  
DR InterPro: IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR008971; HSP40 DnaJ\_pap.  
DR InterPro: IPR003095; Hsp DnaJ.  
DR InterPro: IPR005829; Sug\_transporter.  
DR Pfam: PF00226; DnaJ\_1.  
DR Pfam: PF01556; DnaJ\_C.  
DR Pfam: PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS: PR00625; DnaJ\_CXXCXGKG; 1.  
DR SMART: SM00271; DnaJ\_1.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00636; DnaJ\_1; 1.  
DR PROSITE: PS00076; DnaJ\_2; 1.  
DR PROSITE: PS00637; DnaJ\_CXXCXGKG; 1.

```

DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 381 AA; 42248 MW; 738B5B7C9BD6C111 CRC64;

Query Match          90.1%; Score 73; DB 2; Length 381;
Best Local Similarity 86.7%; Pred. No. 0.00026;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDOYGHAAFE 15
   |||||:|||||
Db 60 QKRAAYDRGHAAFE 74

RESULT 40
DNAME RHOPA
ID DNAME RHOPA STANDARD; PRT; 379 AA.
AC O6NC3.
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocustNames=RPA0334;
OS Rhodopseudomonas palustris
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.B., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris."
RL Nat. Biotechnol. 22:55-61(2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC -----
CC EMBL; BX52594; CAE25778.1; -.
DR PROSITE; PS00636; DNAME_1; 1.
DR PROSITE; PS50076; DNAME_2; 1.
DR PROSITE; PS00637; DNAME_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 7 72 J-domain.
FT DOMAIN 79 118 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).

FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 379 AA; 40992 MW; 53048358B1617B10 CRC64;

Query Match          88.9%; Score 72; DB 1; Length 379;
Best Local Similarity 92.9%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDOYGHAAFE 15
   |||||:|||||
Db 64 KRAAYDRGHAAFE 77

RESULT 41
DNAME RHOS7
ID DNAME RHOS7 STANDARD; PRT; 379 AA.
AC O08356;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Rhodopseudomonas sp. (strain No.7).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=269092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97214635; PubMed=9061015; DOI=10.1016/S0167-4781(96)00222-9;
RA Momma K., Inui M., Yamagata H., Yukawa H.;
RA "Cloning of dnaK and dnaJ homologous genes from a purple non-sulfur
RT bacterium Rhodopseudomonas species."
RL Biochim. Biophys. Acta 1350:235-239(1997).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D78133; BAA19797.1; -.
DR HSPSP; P08622; LBQZ.
DR InterPro; IPR002939; DNAME_C.
DR InterPro; IPR001305; DNAME_CXXCXGKG.
DR InterPro; IPR001623; DNAME_N.
DR InterPro; IPR003095; Hsp DNAME.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DNAME_1.
DR Pfam; PF01556; DNAME_C; 1.
DR Pfam; PF00684; DNAME_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAMEPROTEIN.
DR SMART; SM00271; DNAME_1.
DR PROSITE; PS00636; DNAME_1; 1.
DR PROSITE; PS50076; DNAME_2; 1.
DR PROSITE; PS00637; DNAME_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 7 72 J-domain.
FT DOMAIN 79 118 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).

```

FT METAL 168 168 Zinc 2 (By similarity).  
 FT METAL 187 187 Zinc 2 (By similarity).  
 FT METAL 190 190 Zinc 2 (By similarity).  
 FT METAL 201 201 Zinc 1 (By similarity).  
 FT METAL 204 204 Zinc 1 (By similarity).  
 SQ SEQUENCE 379 AA; 40392 MW; 53049356B1617B10 CRC64;

Query Match 88.9%; Score 72; DB 1; Length 379;  
 Best Local Similarity 92.9%; Pred. No. 0.00038;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15  
 |||||:|||||  
 Db 64 KRAAYDRYGHAAFE 77

RESULT 42  
 Q8RB67 PRELIMINARY; PRT; 384 AA.  
 AC Q8RB67;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Molecular chaperones (Contain C-terminal Zn finger domain).  
 GN Name=DnaJ; OrderedLocusNames=TT0956;  
 OS Thermoanaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
 NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4;  
 RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RT "A complete sequence of the T. tengcongensis genome.";  
 RL Genome Res. 12:689-700(2002).  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AE013061; AM24212.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pdp.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PRINTS; PR00625; DnaJ\_CXXCXGKG; 1.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 384 AA; 42718 MW; 92B39791273F4094 CRC64;

Query Match 88.9%; Score 72; DB 2; Length 384;  
 Best Local Similarity 86.7%; Pred. No. 0.00039;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 |||||:|||||  
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 43  
 Q7VQL3 PRELIMINARY; PRT; 377 AA.  
 AC Q7VQL3;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DnaJ protein.  
 GN Name=dnaJ; OrderedLocusNames=Bf1115;  
 OS Candidatus Blochmannia floridanus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.  
 NCBI\_TaxID=203907;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22784745; PubMed=12886019; DOI=10.1073/pnas.1533499100;  
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,  
 RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,  
 RA van Ham R.C.H.J., Gross R., Moya A.;  
 RT "The genome sequence of Blochmannia floridanus: comparative analysis  
 of reduced genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).  
 DR EMBL; BX248584; CAD83636.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pdp.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 377 AA; 41379 MW; 2047D0E868DB2A9E CRC64;

Query Match 86.4%; Score 70; DB 2; Length 377;  
 Best Local Similarity 80.0%; Pred. No. 0.00085;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 :||:|||||  
 Db 61 EKRSAYDQYGHAAFE 75

RESULT 44  
 ID DnaJ\_PASHA STANDARD; PRT; 379 AA.  
 AC 052065;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN Name=dnaJ;  
 OS Pasteurella haemolytica.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Mannheimia.  
 NCBI\_TaxID=75985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Serotype A1;  
 RA Al S.L., Lo R.Y.C.;  
 RT "The dnaK and dnaJ chaperone genes of Pasteurella haemolytica A1.";  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 CC -!- SIMILARITY: Contains 1 CR domain.  
 CC -!- SIMILARITY: Contains 1 J domain.  
 CC -----  
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 CC -----

CC EMBL; AF017730; AAB94555.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR InterPro; IPR002939; DnaJ C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp DnaJ.  
 DR InterPro; IPR011031; Multihaem\_cyt.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 FT DOMAIN 5 70 J-domain.  
 FT DOMAIN 77 119 Gly-rich.  
 FT REPEAT 149 156 CXXCXGKG motif.  
 FT REPEAT 166 173 CXXCXGKG motif.  
 FT REPEAT 188 195 CXXCXGKG motif.  
 FT REPEAT 202 209 CXXCXGKG motif.  
 FT METAL 149 149 Zinc 1 (By similarity).  
 FT METAL 152 152 Zinc 1 (By similarity).  
 FT METAL 166 166 Zinc 2 (By similarity).  
 FT METAL 169 169 Zinc 2 (By similarity).  
 FT METAL 188 188 Zinc 2 (By similarity).  
 FT METAL 191 191 Zinc 2 (By similarity).  
 FT METAL 202 202 Zinc 1 (By similarity).  
 FT METAL 205 205 Zinc 1 (By similarity).  
 SQ SEQUENCE 379 AA; 41185 MW; 5467F5546219A98D CRC64;

Query Match 86.4%; Score 70; DB 1; Length 379;  
 Best Local Similarity 80.0%; Pred. No. 0.00085;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 :|||:|||||:  
 Db 61 EKXAMYDQYGHAAFE 75

RESULT 45  
 ID DnaJ\_BUCBP STANDARD; PRT; 383 AA.  
 AC Q89AU7;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Chapterone protein dnaJ.  
 GN Name=dnaJ; OrderedLocustNames=bbp141;  
 OS Buchnera aphidicola (subsp. Baizongia pistaciae).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=135842;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12522265; DOI=10.1073/pnas.0235981100;  
 RA van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,  
 Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

RA Tanames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;  
 RT "Reductive genome evolution in Buchnera aphidicola.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grp94,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -!- COPACITOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 CC -!- SIMILARITY: Contains 1 CR domain.  
 CC -!- SIMILARITY: Contains 1 J domain.  
 CC -----

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

CC EMBL; AE014016; AAO26875.1; -.  
 DR HSSP; P08622; 1BQZ.  
 DR InterPro; IPR002939; DnaJ C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp DnaJ.  
 DR InterPro; IPR011031; Multihaem\_cyt.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; FALSE NEG.  
 KW Chapterone; Complete proteome; DNA replication; Heat shock;  
 FT Metal-binding; Repeat; Zinc.  
 FT DOMAIN 5 70 J-domain.  
 FT DOMAIN 77 120 Gly-rich.  
 FT REPEAT 150 157 CXXCXGKG motif.  
 FT REPEAT 167 174 CXXCXGKG motif.  
 FT REPEAT 189 196 CXXCXGKG motif.  
 FT REPEAT 203 210 CXXCXGKG motif.  
 FT METAL 150 150 Zinc 1 (By similarity).  
 FT METAL 153 153 Zinc 1 (By similarity).  
 FT METAL 167 167 Zinc 2 (By similarity).  
 FT METAL 170 170 Zinc 2 (By similarity).  
 FT METAL 189 189 Zinc 2 (By similarity).  
 FT METAL 192 192 Zinc 2 (By similarity).  
 FT METAL 203 203 Zinc 1 (By similarity).  
 FT METAL 206 206 Zinc 1 (By similarity).  
 SQ SEQUENCE 383 AA; 43299 MW; 881F48797684838D CRC64;

Query Match 86.4%; Score 70; DB 1; Length 383;  
 Best Local Similarity 80.0%; Pred. No. 0.00086;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 :|||:|||||:  
 Db 61 KKRTAYDQYGHAAFE 75

RESULT 46  
 ID Q8KYX6 PRELIMINARY; PRT; 382 AA.  
 AC Q8KYX6;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DnaJ protein.  
 GN Name=dnaJ;  
 OS uncultured proteobacterium.  
 OC Bacteria; Proteobacteria; environmental samples.

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EMBL; U57637; AAC45474.1; -.  
HSP; P08622; 1XBL.  
InterPro; IPR02939; DnaJ C.  
InterPro; IPR001305; DnaJ\_CXXCXGKG.  
InterPro; IPR001623; DnaJ\_N.  
InterPro; IPR008971; HSP40\_DnaJ\_pap.  
InterPro; IPR003095; Hsp\_DnaJ.  
InterPro; IPR011031; Multihaem\_cyt.  
Pfam; PF00226; DnaJ; 1.  
Pfam; PF01556; DnaJ C; 1.  
Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
PRINTS; PR00625; DNAJPROTEIN.  
SMART; SM00271; DnaJ; 1.  
PROSITE; PS00636; DnaJ 1; 1.  
PROSITE; PS50076; DnaJ 2; 1.  
PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
DOMAIN 3 72 J-domain.  
FT DOMAIN 76 119 Gly-rich.  
FT REPEAT 156 163 CXXCXGKG motif.  
FT REPEAT 173 180 CXXCXGKG motif.  
FT REPEAT 195 202 CXXCXGKG motif.  
FT REPEAT 209 216 CXXCXGKG motif.  
FT METAL 156 216 Zinc 1 (By similarity).  
FT METAL 159 195 Zinc 1 (By similarity).  
FT METAL 173 173 Zinc 2 (By similarity).  
FT METAL 176 176 Zinc 2 (By similarity).  
FT METAL 195 195 Zinc 2 (By similarity).  
FT METAL 198 198 Zinc 2 (By similarity).  
FT METAL 209 209 Zinc 1 (By similarity).  
FT METAL 212 212 Zinc 1 (By similarity).  
SQ SEQUENCE 384 AA; 40692 MW; 607F94189807470B CRC64;  
Query Match 85.2%; Score 69; DB 1; Length 384;  
Best Local Similarity 85.7%; Pred. No. 0.0013; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 0;  
QY 2 KRAAYDQYGHAAFE 15  
Db 62 KRAAYDRYGHAAFE 75  
:||||:|||||  
:||||:|||||  
RESULT 48  
ID DnaJ ERYRH STANDARD; PRT; 370 AA.  
AC Q05676;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Chaperone protein dnaJ.  
GN Name=dnaJ;  
OS Erysiplothrix rhusiopathiae.  
OC Bacteria; Firmicutes; Mollicutes; Anaeroplasmatales;  
OC Erysiplothrichaceae; Erysiplothrix.  
OX NCBI\_TaxID=1648;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BI-6P;  
RX MEDLINE=93366167; PubMed=8359682; DOI=10.1016/0378-1097(93)90186-6;  
RA Rockabrand D., Partridge J., Krska J., Blum P.;  
RT "Nucleotide sequence analysis and heterologous expression of the  
RT Erysiplothrix rhusiopathiae dnaJ gene."  
RL FEMS Microbiol. Lett. 111:79-85(1993).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).



```

CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; L08110; AAA71922.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; Hsp40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C_1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW DOMAIN 4 72 J-domain.
FT REPEAT 77 106 Gly-rich.
FT REPEAT 147 154 CXXCXGKG motif.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 190 197 CXXCXGKG motif.
FT REPEAT 204 211 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 193 193 Zinc 2 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
FT METAL 207 207 Zinc 1 (By similarity).
SQ SEQUENCE 370 AA; 40331 MW; 9A2B0F0E4546767D CRC64;

Query Match 84.0%; Score 68; DB 1; Length 370;
Best Local Similarity 80.0%; Pred. No. 0.0019;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 61 OKRANYDQFGHAAFD 75

RESULT 49
DnaJ_BRAJA STANDARD; PRT; 377 AA.
AC P94319;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
GN Names=dnaJ; OrderedLocustNames=blr0680;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_taxid=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110spc4;
RX MEDLINE=97261868; PubMed=9108282; DOI=10.1007/s004380050408;
RA Minder A.C., Narberhaus F., Babet M., Hennecke H., Fischer H.-M.;

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RT "The dnaKJ operon belongs to the sigma32-dependent class of heat shock
RT genes in Bradyrhizobium japonicum.";
RL Mol. Genet. 254:195-206(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; Y09633; CAA70848.1; -.
CC HSP; P08622; 1BQZ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C_1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 8 73 J-domain.
FT REPEAT 79 118 Gly-rich.
FT REPEAT 148 155 CXXCXGKG motif.
FT REPEAT 165 172 CXXCXGKG motif.
FT REPEAT 187 194 CXXCXGKG motif.
FT REPEAT 201 208 CXXCXGKG motif.
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 151 151 Zinc 1 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 168 168 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 190 190 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
FT METAL 204 204 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 40945 MW; 7FE38A8EBC9B1BAA CRC64;

Query Match 84.0%; Score 68; DB 1; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.0019;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
DB 65 KRAAYDQFGHAAFE 78

```



## RESULT 50

DNAJ\_METSS STANDARD; PRT; 371 AA.  
AC Q92PFC5;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
GN Name=dnaJ;  
OS Methylovorus sp. (strain SS1 / DSM 11726).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;  
OC Methylophilaceae; Methylovorus.  
OX NCBI\_TaxID=81683;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Eom C.Y., Kim Y.M.;  
RT "grpE, dnaK, and dnaJ genes of Methylovorus sp. strain SS1 DSM11726.";  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
CC -!- SIMILARITY: Contains 1 CR domain.  
CC -!- SIMILARITY: Contains 1 J domain.  
CC  
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CC  
CC -----  
EMBL; AF106835; AAC95379.1; --  
DR HSSP; P08622; 1BQZ.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR InterPro; IPR011031; Multithaem\_cyt.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
FT DOMAIN 5 70  
FT J-domain.  
FT DOWAIN 79 115  
FT Gly-rich.  
FT REPEAT 145 152  
FT CXXCXGKG motif.  
FT REPEAT 162 169  
FT CXXCXGKG motif.  
FT REPEAT 184 191  
FT CXXCXGKG motif.  
FT REPEAT 198 205  
FT CXXCXGKG motif.  
FT METAL 145 145  
FT Zinc 1 (By similarity).  
FT METAL 148 148  
FT Zinc 2 (By similarity).  
FT METAL 162 162  
FT Zinc 2 (By similarity).  
FT METAL 165 165  
FT Zinc 2 (By similarity).  
FT METAL 184 184  
FT Zinc 2 (By similarity).  
FT METAL 187 187  
FT Zinc 2 (By similarity).  
FT METAL 198 198  
FT Zinc 1 (By similarity).  
FT METAL 201 201  
FT Zinc 1 (By similarity).  
SQ SEQUENCE 371 AA; 41052 MW; 86C1AF58F87CF95C CRC64;

Query Match 82.7%; Score 67; DB 1; Length 371;

Best Local Similarity 80.0%; Pred. No. 0.0028;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAGVD 75

## RESULT 51

O62HD6 PRELIMINARY; PRT; 376 AA.  
ID Q62HD6;  
AC Q62HD6;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
GN Name=dnaJ; ORFNames=BNA2325;  
OS Burkholderia mallei ATCC 23344.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia.  
OX NCBI\_TaxID=243160;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=ATCC 23344;  
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,  
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,  
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,  
RA Gwinn M.L., Haft D.H., Khouiri H., Kolonay J.F., Madupu R.,  
RA Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,  
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,  
RA Zhou L., Fraser C.M.;  
RT "Structural flexibility in the Burkholderia mallei genome.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).  
DR EMBL; CP000010; NAU49785.1; --  
SQ SEQUENCE 376 AA; 40549 MW; 9C894B4235A35D31 CRC64;

Query Match 82.7%; Score 67; DB 2; Length 376;

Best Local Similarity 80.0%; Pred. No. 0.0028;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15

Db 61 QKRAAYDQYGHAGVD 75

## RESULT 52

O63R47 PRELIMINARY; PRT; 376 AA.  
ID Q63R47;  
AC Q63R47;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative DnaJ chaperone protein.  
GN Name=dnaJ; ORFNames=BPS42826;  
OS Burkholderia pseudomallei K96243.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia.  
OX NCBI\_TaxID=272560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=K96243;  
RX PubMed=15377794;  
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,  
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., I.R.,  
RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,  
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,  
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,  
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,  
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,  
RA Rabinowitch E., Rutherford K., Sanders M., Simmonds M.,  
RA Songvilal S., Stevens K., Tumapa S., Vesaratchaveh M.,  
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.P., Parkhill J.;  
RT "Genomic plasticity of the causative agent of melioidosis,  
RT Burkholderia pseudomallei.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).  
DR EMBL; BX571965; CHA36836.1; --  
SQ SEQUENCE 376 AA; 40596 MW; E462930B1205004E CRC64;

Query Match 82.7%; Score 67; DB 2; Length 376;

Best Local Similarity 80.0%; Pred. No. 0.0028; 2; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1;

QY 1 QKRAAYDQYGHAAFE 15  
| | | | | | | | | | | | | | | |  
Db 61 QKRAAYDQYGHAGVD 75

## RESULT 53

ID\_DNAJ\_LACSK STANDARD; PRT; 383 AA.  
AC O87778;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Chapterone protein dnaJ.  
GN Name=dnaJ;  
OS Lactobacillus sakei.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1599;  
[1]  
RN RP SEQUENCE FROM N.A.  
RC STRAIN=LTH681.  
RX MEDLINE=20020854; PubMed=10553284;  
RA Schmidt G., Hertel C., Hammes W.P.;  
RT "Molecular characterisation of the dnaK operon of Lactobacillus sakei LTH681";  
RL Syst. Appl. Microbiol. 22:321-328(1999).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- INDUCTION: By heat shock as well as salt or ethanol stress.  
CC -1- SIMILARITY: Belongs to the dnaJ family.  
CC -1- SIMILARITY: Contains 1 CR domain.  
CC -1- SIMILARITY: Contains 1 J domain.

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CC EMBL; AJ006274; CAA06942.1; -.  
DR HSSP; P08622; 1XBL.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pep.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR InterPro; IPR011031; Multihaem\_cyt.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PS00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS50076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
FT DOMAIN 6 70 J-domain.  
FT DOMAIN 73 123 Gly-rich.  
FT REPEAT 153 160 CXXCXGKG motif.  
FT REPEAT 170 177 CXXCXGKG motif.  
FT REPEAT 196 203 CXXCXGKG motif.  
FT REPEAT 210 217 CXXCXGKG motif.  
FT REPEAT 216 217 CXXCXGKG motif.  
FT METAL 153 153 Zinc 1 (By similarity).  
FT METAL 156 156 Zinc 1 (By similarity).  
FT METAL 170 170 Zinc 2 (By similarity).  
FT METAL 173 173 Zinc 2 (By similarity).

FT METAL 196 196 Zinc 2 (By similarity).  
FT METAL 199 199 Zinc 2 (By similarity).  
FT METAL 210 210 Zinc 1 (By similarity).  
FT METAL 213 213 Zinc 1 (By similarity).  
SQ SEQUENCE 383 AA; 41132 MW; 3D71B3C4419EAF59 CRC64;

Query Match 81.5%; Score 66; DB 1; Length 383;  
Best Local Similarity 100.0%; Pred. No. 0.0044; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0;

QY 1 QKRAAYDQYGHGA 12  
| | | | | | | | | | | | | | | |  
Db 61 QKRAAYDQYGHGA 72

## RESULT 54

Q93R26 PRELIMINARY; PRT; 386 AA.  
AC Q93R26;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ.  
GN Name=dnaJ;  
OS Tetragenococcus halophilus (Pediococcus halophilus).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;  
OC Tetragenococcus.  
OX NCBI\_TaxID=51669;  
[1]  
RN RP SEQUENCE FROM N.A.  
RA Fukuda D., Watanabe M., Sonezaki S., Sugimoto S., Sonomoto K., Ishizaki A.;  
RT "Molecular characterization and regulatory analysis of dnaK operon of halophilic lactic acid bacterium Tetragenococcus halophilus";  
RL J. Biosci. Bioeng. 0:0-0(2002).  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AB070346; BAB63291.1; -.  
DR HSSP; P08622; 1XBL.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006240; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pep.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PS00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
DR PROSITE; PS50076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 386 AA; 41938 MW; 1F7FB80973AC02D9 CRC64;

Query Match 81.5%; Score 66; DB 2; Length 386;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHGA 12  
| | | | | | | | | | | | | | | |  
Db 61 QKRAAYDQYGHGA 72

## RESULT 55

```
Q8D2Q6
ID Q8D2Q6 PRELIMINARY; PRT; 374 AA.
AC Q8D2Q6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocusNames=WIGBR2980;
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=36870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091; DOI=10.1038/ng986;
RA Aknan L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Akoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia.";
RL Nat. Genet. 32:402-407(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AB063522; BAC24444.1; -.
CC HSP; P08622; IBOZ.
CC GO; GO:0051082; P:unfolded protein binding; IEA.
CC GO; GO:0006457; P:protein folding; IEA.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40 DnaJ_p.
CC InterPro; IPR003095; Hsp_DnaJ.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC SMART; SM00625; DnaJPROTEIN.
CC QW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 374 AA; 41467 MW; 279CA4EC5AB020A7 CRC64;

Query Match 80.2%; Score 65; DB 2; Length 374;
Best Local Similarity 73.3%; Pred. No. 0.0064;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
Db 61 KGRAAYNQYGHATFD 75
:|||||:|||||:
:|||||:|||||:

RESULT 56
DnaJ_RICPR STANDARD; PRT; 370 AA.
AC Q92DYO;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=RP184;
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX STAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alismark U.C.M., Podowski R.M., Naeslund A.K.,
```

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RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; AJ235270; CAA14650.1; -.
CC PIR; C71729; C71729.
CC HSP; P08622; IBOZ.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; P00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC Chaperone; Complete proteome; DNA replication; Heat shock;
CC Metal-binding; Repeat; Zinc.
CC DOMAIN 2 70 J-domain.
CC FT DOMAIN 79 105 Gly-rich.
CC FT REPEAT 146 153 CXXCXGKG motif.
CC FT REPEAT 163 170 CXXCXGKG motif.
CC FT REPEAT 185 192 CXXCXGKG motif.
CC FT REPEAT 199 206 CXXCXGKG motif.
CC FT METAL 146 146 Zinc 1 (By similarity).
CC FT METAL 149 149 Zinc 1 (By similarity).
CC FT METAL 163 163 Zinc 2 (By similarity).
CC FT METAL 166 166 Zinc 2 (By similarity).
CC FT METAL 185 185 Zinc 2 (By similarity).
CC FT METAL 188 188 Zinc 2 (By similarity).
CC FT METAL 199 199 Zinc 1 (By similarity).
CC FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 370 AA; 41013 MW; AE6721285B4F6186 CRC64;

Query Match 79.0%; Score 64; DB 1; Length 370;
Best Local Similarity 73.3%; Pred. No. 0.0094;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAPE 15
Db 59 QKRAAYDREGHDAFQ 73
:|||||:|||||:
:|||||:|||||:

RESULT 57
Q68XI3 PRELIMINARY; PRT; 370 AA.
ID Q68XI3;
AC Q68XI3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=RT0175;
OS Rickettsia typhi.
```

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 RN NCBI\_TaxID=785;  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=Wilington.  
 RX PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;  
 RA McLeod M.P., Qin X., Karpach S.E., Gioia J., Highlander S.K.,  
 RA Fox G.E., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C.,  
 RA Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G.,  
 RA Gibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstein G.M.,  
 RT "Complete genome sequence of Rickettsia typhi and comparison with  
 RT sequences of other Rickettsiae.";  
 RL J. Bacteriol. 186:5842-5855(2004).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 CC EMBL; AE017197; AAU03659.1; -.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 370 AA; 41145 MW; 15265F965A5DD09 CRC64;

Query Match 79.0%; Score 64; DB 2; Length 370;  
 Best Local Similarity 73.3%; Pred. No. 0.0094;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 |||||:|||||  
 DB 59 QKRAAYDRFGHDAFQ 73

RESULT 58  
 QBRH03  
 ID QBRH03 PRELIMINARY; PRT; 392 AA.  
 AC QBRH03;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN OrderedLocustNames=FN0118;  
 OS Fusobacterium nucleatum (subsp. nucleatum).  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=76856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 25586;  
 RX MEDLINE=21886394; PubMed=11889109;  
 RX DOI=10.1128/JB.184.7.2005-2018.2002;  
 RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltman E., Bernal A.,  
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,  
 RA Fonstein M., Kyrpides N.C., Overbeek R.,  
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
 RT nucleatum strain ATCC 25586.";  
 RL J. Bacteriol. 184:2005-2018(2002).  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; AE010525; AAL94327.1; -.  
 DR HSP; P08622; lBQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 KW Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 392 AA; 42973 MW; E62392DBE8338AD6 CRC64;

Query Match 79.0%; Score 64; DB 2; Length 392;  
 Best Local Similarity 73.3%; Pred. No. 0.01;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15  
 |||||:|||||  
 DB 66 QKQYDQFGHAAFE 80

RESULT 59  
 Q7P753  
 ID Q7P753 PRELIMINARY; PRT; 393 AA.  
 AC Q7P753;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN Name=FN1498;  
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=209882;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 49256;  
 RA Kapral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,  
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,  
 RA Haselkorn R., Overbeek R., Kyrpides N.,  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the dnaJ family.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AABF01000021; EAA24657.1; -.  
 DR HSP; P08622; lBQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006280; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.

DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 393 AA; 42993 MW; B644C4A54E05611 CRC64;

Query Match 79.0%; Score 64; DB 2; Length 393;  
 Best Local Similarity 73.3%; Pred. No. 0.01;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 ||:|||||  
 Db 66 QKKQYDQFGHAAFE 80

RESULT 60  
 Q6SET1 PRELIMINARY; PRT; 367 AA.  
 AC Q6SET1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chaperone protein DnaJ.  
 GN Name=dnaJ; ORFNames=EBAC750-10A10.17;  
 OS uncultured bacterium 583.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=257403;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA DeLong E.F.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Heidelberg J.F.; Eisen J.A.; Nelson W.C.; DeLong E.F.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AY458650; AAR38491.1; -  
 DR GO; GO:0051082; P:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR00345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR EMBL; AY458650; AAR38491.1; -  
 DR GO; GO:0051082; P:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR00345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 367 AA; 39803 MW; PF0983B53CADC6C1 CRC64;

Query Match 77.8%; Score 63; DB 2; Length 367;  
 Best Local Similarity 73.3%; Pred. No. 0.014;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
 ||:|||||  
 Db 62 QKRSAYDQFGHAGVE 76

RESULT 61  
 Q6SGG2 PRELIMINARY; PRT; 369 AA.  
 AC Q6SGG2;  
 DT 03-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chaperone protein DnaJ.  
 GN Name=dnaJ; ORFNames=EBAC750-16D01.42;  
 OS uncultured bacterium 560.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=257395;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA DeLong E.F.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Heidelberg J.F.; Eisen J.A.; Nelson W.C.; DeLong E.F.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AY458642; AAR37900.1; -  
 DR GO; GO:0051082; P:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR00345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 369 AA; 39926 MW; 75616D70958FF8C1 CRC64;  
 Query Match 77.8%; Score 63; DB 2; Length 369;  
 Best Local Similarity 73.3%; Pred. No. 0.014;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QKRAAYDQYGHAAFE 15  
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 Db 62 QKRSAYDQFGHAGVE 76

RESULT 62  
 Q7WG15 PRELIMINARY; PRT; 373 AA.  
 AC Q7WG15;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Molecular chaperone.  
 GN Name=dnaJ; OrderedLocustNames=BB3933;  
 OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RB50 / ATCC BAA-588;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

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RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640449; CAE34296.1; -.
DR HSSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C_1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; FALSE NEG.
KW Complete proteome.
SQ SEQUENCE 373 AA; 40249 MW; 10899CE97B119B7F CRC64;

Query Match 77.8%; Score 63; DB 2; Length 373;
Best Local Similarity 73.3%; Pred. No. 0.014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 61 QKRAAYDRYGHAGVD 75

RESULT 63
DNJ2_AQUAE STANDARD; PRT; 376 AA.
AC 066921;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ-2.
GN Name=dnaJ2; OrderedLocusNames=AQ_703;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]_TaxID=63363;
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AE000703; AAC06881.1; -.
DR PIR; E70361; E70361.
DR HSSP; P08622; 1XBL.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hep_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C_1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; FALSE NEG.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 8 72 J-domain.
FT REPEAT 156 163 CXXCXGKG motif.
FT REPEAT 172 179 CXXCXGKG motif.
FT REPEAT 194 201 CXXCXGKG motif.
FT REPEAT 207 214 CXXCXGKG motif.
FT METAL 156 156 Zinc 1 (By similarity).
FT METAL 159 159 Zinc 1 (By similarity).
FT METAL 172 172 Zinc 2 (By similarity).
FT METAL 175 175 Zinc 2 (By similarity).
FT METAL 194 194 Zinc 2 (By similarity).
FT METAL 197 197 Zinc 2 (By similarity).
FT METAL 207 207 Zinc 1 (By similarity).
FT METAL 210 210 Zinc 1 (By similarity).
SQ SEQUENCE 376 AA; 41963 MW; 9C8FBFB29A8A016D CRC64;

Query Match 77.8%; Score 63; DB 1; Length 376;
Best Local Similarity 73.3%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DB 63 EKRLYDMYGHAAFE 77

RESULT 64
QW520 PRELIMINARY; PRT; 377 AA.
ID QW520;
AC QW520;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molecular chaperone.
GN Name=dnaJ; OrderedLocusNames=BPP3484;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]_TaxID=519;
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

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RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica.";  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640433; CAE38768.1; --  
DR HSSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolding protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; CytC\_heme\_BS.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C\_1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C\_1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Complete proteome.  
SQ SEQUENCE 377 AA; 40551 MW; 8AE63FF201B410B5 CRC64;  
  
Query Match 77.8%; Score 63; DB 2; Length 377;  
Best Local Similarity 73.3%; Pred. No. 0.014;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 QKRAAYDQYGHAFPE 15  
|||||:||||:  
Db 61 QKRAAYDRYGHAGVD 75  
  
RESULT 65  
ID DnaJ LEGPN STANDARD; PRT; 379 AA.  
AC P50025;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Chaperone protein dnaJ.  
GN Name=dnaJ;  
OS Legionella pneumophila.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Legionellaceae; Legionella.  
OX NCBI\_TaxID=446;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JR32;  
RA Sadosky A.B., Shuman H.A.;  
RT "Characterization of the Legionella pneumophila heat shock gene  
RT cluster containing grps, dnaK and dnaJ";  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grps,  
CC the ATPase activity of dnaK (By similarity).  
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
CC -!- SIMILARITY: Contains 1 CR domain.  
CC -!- SIMILARITY: Contains 1 J domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U15010; AAA80278.1; --  
DR HSSP; P08622; 1BQZ.

DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR InterPro; IPR011031; Multihem\_cyt.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C\_1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
FT DOMAIN 5 70  
FT Gly-rich.  
FT REPEAT 73 110  
FT CXXCXGKG motif.  
FT REPEAT 148 155  
FT CXXCXGKG motif.  
FT REPEAT 165 172  
FT CXXCXGKG motif.  
FT REPEAT 187 194  
FT CXXCXGKG motif.  
FT REPEAT 201 208  
FT CXXCXGKG motif.  
FT METAL 148 148  
FT Zinc 1 (By similarity).  
FT METAL 151 151  
FT Zinc 1 (By similarity).  
FT METAL 165 165  
FT Zinc 2 (By similarity).  
FT METAL 168 168  
FT Zinc 2 (By similarity).  
FT METAL 187 187  
FT Zinc 2 (By similarity).  
FT METAL 190 190  
FT Zinc 2 (By similarity).  
FT METAL 201 201  
FT Zinc 1 (By similarity).  
FT METAL 204 204  
FT Zinc 1 (By similarity).  
SQ SEQUENCE 379 AA; 41279 MW; 2611F594CDBFF58 CRC64;  
  
Query Match 77.8%; Score 63; DB 1; Length 379;  
Best Local Similarity 73.3%; Pred. No. 0.014;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 QKRAAYDQYGHAFPE 15  
|||||:||||:  
Db 61 QKRAAYDRYGHAGVD 75  
  
RESULT 66  
ID Q7VVY3 PRELIMINARY; PRT; 385 AA.  
AC Q7VVY3;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molecular chaperone.  
GN Name=dnaJ; OrderedLocNames=BP2498;  
OS Bordetella pertussis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
OX NCBI\_TaxID=520;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;  
RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Chervach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica.";  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640418; CAE42770.1; --  
DR HSSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolding protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.

Qy 2 KRAAYDQYGHAAFE 15



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Db      62 KRAAYDQYGHAGVD 75
|||||
RESULT 69
DNAME_PSEAE STANDARD; PRT; 377 AA.
AC Q9HV44;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaJ.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K.; Pham X.-Q.T.; Erwin A.L.; Mizoguchi S.D.; Warren P.;
RA Hickey M.J.; Brinkman F.S.L.; Hufnagle W.O.; Kowalik D.J.; Lagrou M.;
RA Garber R.L.; Coltry L.; Tolentino E.; Westbrook-Wadman S.; Yuan Y.;
RA Brody L.L.; Coulter S.N.; Folger K.R.; Kas A.; Larbig K.; Lim R.M.;
RA Smith K.A.; Spencer D.H.; Wong G.K.-S.; Wu Z.; Paulsen I.T.;
RA Reizer J.; Saier M.H.; Hancock R.E.W.; Lory S.; Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE004889; AAC08146.1; -.
DR PIR; A83052; A83052.
DR HSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70 J-domain.
FT DOMAIN 73 119 Gly-rich.
FT REPEAT 149 156 CXXCXGKG motif.
FT REPEAT 166 173 CXXCXGKG motif.
FT REPEAT 188 195 CXXCXGKG motif.
FT REPEAT 202 209 CXXCXGKG motif.
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 152 152 Zinc 1 (By similarity).

Query Match 76.5%; Score 62; DB 1; Length 377;
Best Local Similarity 78.6%; Pred.No. 0.022;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAFPE 15
|||||
Db 62 KRAAYDQYGHAGVD 75

RESULT 70
Q87WPI PRELIMINARY; PRT; 380 AA.
AC Q87WPI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DnaJ protein.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R.; Joardar V.; Lindeberg M.; Selengut J.; Paulsen I.T.;
RA Gwinn M.L.; Dodson R.J.; DeBoy R.T.; Durkin A.S.; Kolonay J.F.;
RA Madupu R.; Daugherty S.C.; Brinkac L.M.; Beanan M.J.; Haft D.H.;
RA Nelson W.C.; Davidson T.M.; Zafar N.; Zhou L.; Liu J.; Yuan Q.;
RA Khouri H.M.; Pedrosa N.B.; Tran B.; Russell D.; Berry K.J.;
RA Uterback T.R.; Van Aken S.E.; Feldblyum T.V.; D'Ascenzo M.;
RA Deng W.-L.; Ramos A.R.; Alfano J.R.; Cartinhour S.; Chatterjee A.K.;
RA Delaney T.P.; Lazarowitz S.G.; Martin G.B.; Schneider D.J.; Tang X.;
RA Bender C.L.; White O.; Fraser C.M.; Collmer A.;
RA "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE016872; AAC057952.1; -.
DR HSP; P08622; 1EXK.
DR TIGR; PSPT04504; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

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DR EMBL; AJ512795; CAD55138.1; --  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 DR SEQUENCE 394 AA; 43153 MW; 7711DA9A629928CD CRC64;  
 Query Match 75.3%; Score 61; DB 2; Length 394;  
 Best Local Similarity 66.7%; Pred. No. 0.034;  
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 QKRAAYDQYGHAAPE 15  
 : : : : :  
 Db 66 EKQYQYDQYGHAAPE 80

RESULT 74  
 Q7PAYO PRELIMINARY; PRT; 373 AA.  
 ID Q7PAYO  
 AC Q7PAYO;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DnaJ protein.  
 GN Name=sib orf. 471;  
 OS Rickettsia sibirica.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsia; Rickettsia.  
 OC NCBI\_TaxID=35793;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Malek J.A., Eremeeva M.E., Dasch G.A.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABW01000001; ERA25704.1; --  
 DR HSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.

DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 DR SEQUENCE 373 AA; 41131 MW; 1A0C23B6E0A2A54D CRC64;  
 Query Match 74.1%; Score 60; DB 2; Length 373;  
 Best Local Similarity 73.3%; Pred. No. 0.048;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 QKRAAYDQYGHAAPE 15  
 : : : : :  
 Db 59 QKRAAYDRLGHDAFQ 73

RESULT 75  
 Q92J37 PRELIMINARY; PRT; 373 AA.  
 ID Q92J37  
 AC Q92J37;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DnaJ protein.  
 GN Name=dnaJ; OrderedLocusNames=RC0232;  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsia; Rickettsia.  
 OC NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
 RL Science 293:2093-2098(2001).  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC EMBL; AE008590; AAL02770.1; --  
 DR PIR; H97728; H97728.  
 DR HSP; P08622; 1BQZ.  
 DR GO; GO:0003576; F:nucleic acid binding; IEA.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; Hsp40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR InterPro; IPR001878; Znf\_CCHC.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR KW Chaperone; Complete proteome; DNA replication; Heat shock;  
 DR Metal-binding; Repeat; Zinc.  
 DR SEQUENCE 373 AA; 41131 MW; 1A0C23B6E0A2A54D CRC64;  
 Query Match 74.1%; Score 60; DB 2; Length 373;  
 Best Local Similarity 73.3%; Pred. No. 0.048;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 QKRAAYDQYGHAAFE 15
Db 59 QKRAAYDRGLGHDAFQ 73

RESULT 76
Q8PMA9
ID Q8PMA9 PRELIMINARY; PRT; 375 AA.
AC Q8PMA9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocusNames=XAC1523;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AB011784; AAM36392.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolds protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00684; DnaJ_CXXCXGXG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00076; DnaJ_2; 1.
DR Chaperone; Complete proteome: DNA replication; Heat shock;
DR Metal-binding; Repeat; Zinc.
SQ SEQUENCE 375 AA; 40317 MW; E6ACA4E70FB8BEC CRC64;

Query Match 74.1%; Score 60; DB 2; Length 375;
Best Local Similarity 78.6%; Pred. No. 0.048;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 62 KRAYDAHGHAAFE 75

RESULT 78
Q8PAK8
ID Q8PAK8 PRELIMINARY; PRT; 376 AA.
AC Q8PAK8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocusNames=XCC1475;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 74.1%; Score 60; DB 2; Length 376;
Best Local Similarity 78.6%; Pred. No. 0.048;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 62 KRAYDAHGHAAFE 75
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RC STRAIN-ATCC 33913 / NCPPB 528;  
 RX MEDLINE=20202145; PubMed=1204217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,  
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Cispina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Fawcighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Mendes J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities."  
 RL Nature 417:459-463(2002).  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; AE012248; AA040771.1; -.  
 DR HSPSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pep.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ\_1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SMO0271; DnaJ; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR Chaperone; Complete proteome; DNA replication; Heat shock;  
 KW Metal-binding; Repeat; Zinc.  
 SQ SEQUENCE 376 AA; 40530 MW; 5B3EC953EACEAF2A CRC64;  
 Query Match 74.1%; Score 60; DB 2; Length 376;  
 Best Local Similarity 78.6%; Pred. No. 0.048;  
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 KRAAYDQYGHAAFE 15  
 DB |||||:||||| 75  
 62 KRAYDAHGHAAFE 75  
 RESULT 79  
 Q7UN96 PRELIMINARY; PRT; 391 AA.  
 AC Q7UN96;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Chaperone protein DnaJ  
 GN Name=dnaJ; OrderedLocusNames=RB8972;  
 OS Rhodospirillum rubrum  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula  
 OX NCBI\_TaxID=117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;

RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
 RA Schleier H., Amann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 RT strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 DR EMBL; BX294148; CAD76021.1; -.  
 DR HSPSP; P08622; 1BQZ.  
 DR GO; GO:0051082; F:unfolded protein binding; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pep.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR SMART; SMO0271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 391 AA; 42391 MW; 49142FA922B65310 CRC64;  
 Query Match 74.1%; Score 60; DB 2; Length 391;  
 Best Local Similarity 78.6%; Pred. No. 0.05;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 KRAAYDQYGHAAFE 15  
 DB |||||:||||| 76  
 63 KRAYDQYGHAAFE 76  
 RESULT 80  
 DNAJ\_CXXBU STANDARD; PRT; 374 AA.  
 AC P42381;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DT Chaperone protein dnaJ.  
 GN Name=dnaJ; OrderedLocusNames=CBU1289;  
 OS Coxiella burnetii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Coxiellaceae; Coxiella.  
 OX NCBI\_TaxID=777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nine Mile;  
 RX MEDLINE=95129924; PubMed=7828937; DOI=10.1016/0378-1119(94)00687-N;  
 RA Zuber M., Hoover T.A., Court D.L.;  
 RT "Cloning, sequencing and expression of the dnaJ gene of Coxiella  
 RT burnetii.";  
 RL Gene 152:99-102(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nine Mile Phase I / RSA 493;  
 RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;  
 RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,  
 RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Bean M.J.,  
 RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,  
 RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,  
 RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;  
 RT "Complete genome sequence of the Q-fever pathogen, Coxiella  
 RT burnetii.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
 CC the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 CC -1- SIMILARITY: Contains 1 CR domain.  
 CC -1- SIMILARITY: Contains 1 J domain.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; L36455; AAA65100.1; -;  
DR EMBL; AE016964; AAO90795.1; -;  
DR PIR; I40843; I40843.  
DR HSP; P08622; IBQZ.  
DR TIGR; CBUL289; -;  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR InterPro; IPR011031; Multihaem\_cyt.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF0684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; zinc.  
FT DOMAIN 5 70 J-domain.  
FT REPEAT 79 109 Gly-rich.  
FT REPEAT 146 153 CXXCXGKG motif.  
FT REPEAT 162 169 CXXCXGKG motif.  
FT REPEAT 184 191 CXXCXGKG motif.  
FT REPEAT 198 205 CXXCXGKG motif.  
FT METAL 146 146 Zinc 1 (By similarity).  
FT METAL 149 149 Zinc 1 (By similarity).  
FT METAL 162 162 Zinc 2 (By similarity).  
FT METAL 165 165 Zinc 2 (By similarity).  
FT METAL 184 184 Zinc 2 (By similarity).  
FT METAL 187 187 Zinc 2 (By similarity).  
FT METAL 198 198 Zinc 1 (By similarity).  
FT METAL 201 201 Zinc 1 (By similarity).  
FT CONFLICT 365 374 DSVKDFTSK -> GTV (in Ref. 1).  
SQ SEQUENCE 374 AA; 40856 MW; 7A9C3F0D140CAF99 CRC64;

Query Match 72.8%; Score 59; DB 1; Length 374;  
Best Local Similarity 66.7%; Pred. No. 0.072;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 OKRAAYDQYGHAAFE 15  
Db 61 RKRASYDQFGHAGVE 75

## RESULT 81

ID Q7NX11 PRELIMINARY; PRT; 375 AA.  
AC Q7NX11;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE Heat shock protein dnaJ; chaperone with DnaK.  
GN Name=dnaJ; OrderedLocusNames=CV1645;  
OS Chromobacterium violaceum.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Chromobacterium.  
OX NCBI\_TaxID=536;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 12472 / DSM 30191;  
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;

RA Vasconcelos A.T.R.; de Almeida D.F.; Hungria M.; Guimaraes C.T.;  
RA Antonio R.V.; Almeida F.C.; de Almeida L.G.P.; de Almeida R.;  
RA Alves-Gomes J.A.; Andrade E.M.; Araripe J.; de Araujo M.F.F.;  
RA Ascoli-Filho S.; Azevedo V.; Baptista A.J.; Bataus L.A.M.;  
RA Batista J.S.; Belo A.; van den Berg C.; Bogo M.; Bonatto S.;  
RA Bordignon J.; Brígido M.M.; Brito C.A.; Brocchi M.; Burity H.A.;  
RA Canargo A.A.; Cardoso D.D.P.; Carneiro N.P.; Carraro D.M.;  
RA Creczynski-Pasa T.B.; Cunha-Junior N.C.; Fagundes N.; Falcao C.L.;  
RA Fantinatti F.; Farias I.P.; Felipe M.S.S.; Ferrari L.P.; Ferro J.A.;  
RA Fazzinelli R.T.; Gomes E.A.; Goncalves P.R.; Grangeiro T.B.;  
RA Grattapaglia D.; Grisard E.C.; Hanna E.S.; Jardim S.N.; Laurino J.;  
RA Leol L.C.T.; Lima L.F.A.; Loureiro M.F.; Lyra M.C.C.P.;  
RA Madeira H.M.F.; Manfio G.P.; Maranhao A.Q.; Martins W.S.;  
RA di Mauro S.M.Z.; de Medeiros S.R.B.; Melssner R.V.; Moreira M.A.M.;  
RA Nascimento F.F.; Nicolas M.F.; Oliveira J.G.; Oliveira S.C.;  
RA Paixao R.P.C.; Parente J.A.; Pedrosa F.O.; Pena S.D.J.; Pereira J.O.;  
RA Pereira M.; Pinto L.S.R.C.; Pinto L.S.; Porto J.I.R.; Potrich D.P.;  
RA Ramalho-Neto C.E.; Reis A.M.M.; Rigo L.U.; Rondinelli E.;  
RA Santos E.B.P.; Santos F.R.; Schneider M.P.C.; Seunaez H.N.;  
RA Silva A.M.R.; da Silva A.L.C.; Silva D.W.; Silva R.; Simoes I.C.;  
RA Simon D.; Soares C.M.A.; Soares R.B.A.; Souza E.M.; Souza K.R.L.;  
RA Souza R.C.; Steffens M.B.R.; Steindel M.; Teixeira S.R.; Urmenyi T.;  
RA Vettore A.; Wassem R.; Zaha A.; Simpson A.J.G.;  
RT "The complete genome sequence of Chromobacterium violaceum reveals  
RT remarkable and exploitable bacterial adaptability.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grps,  
CC the ATPase activity of dnaK (By similarity).  
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AE016915; AAO5921.1; -;  
DR HSSP; P08622; IBQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR PRINTS; PR00625; DnaJ\_CXXCXGKG; 1.  
DR PROSITE; PS00625; DnaJPROTEIN.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; zinc.  
SQ SEQUENCE 375 AA; 40538 MW; E4D171B33B7EE433 CRC64;

Query Match 72.8%; Score 59; DB 2; Length 375;  
Best Local Similarity 66.7%; Pred. No. 0.072;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15

Db 61 QKRGYDQFGHAGVD 75

## RESULT 82

ID Q8XW41 PRELIMINARY; PRT; 380 AA.  
AC Q8XW41;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE PROBABLE CHAPERONE PROTEIN.  
GN Name=dnaJ; Synonym=RS04588; OrderedLocusNames=RS02634;  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
CC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;  
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangelot S.,  
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
RA Chantier M., Choise N., Claudel-Renard C., Cunac S., Demange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,  
RA Weissenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";  
RL Nature 415:497-502(2002).  
CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -|- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AL646071; CAD16341.1; -;  
DR HSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR Pfam; PF00228; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_2.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 380 AA; 41460 MW; D340150445330340 CRC64;  
  
Query Match 72.8%; Score 59; DB 2; Length 380;  
Best Local Similarity 71.4%; Pred. No. 0.073;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 KRAAYDQYGHAF 15  
Db 62 KRAAYDQYGHAGVD 75  
||||| :  
RESULT 83  
ID Q88DU3 PRELIMINARY; PRT; 375 AA.  
AC Q88DU3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein.  
GN Name=dnaJ; OrderedLocusNames=PP4726;  
OS Pseudomonas putida (strain KT2440).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
CC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=160488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=22423060; PubMed=12534463;  
RX Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
RA Martins dos Santos V.A.P., Fouts D.E., Fouts S.R., Pop M., Holmes M.,  
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,  
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,  
RA Hance I., Chris Lee P., Holtzapfle B.K., Scanlan D., Tran K.,  
RA Moazzaz A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,  
RA Kiewitz C., Eisen J.A., Timmis K.N., Duisterhoef A., Tuemmler B.,  
RA Fraser C.M.;  
RT "Complete genome sequence and comparative analysis of the  
RT metabolically versatile Pseudomonas putida KT2440.";  
RL Environ. Microbiol. 4:799-808(2002).  
CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -|- SIMILARITY: Belongs to the dnaJ family.  
DR EMBL; AE016791; AAN70298.1; -;  
DR HSP; P08622; 1BQZ.  
DR TIGR; PP4726; -;  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006260; P:DNA replication; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR00345; CytC heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pep.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00636; DnaJ\_1; UNKNOWN\_1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 375 AA; 40181 MW; BA864E70768BCSAC CRC64;  
  
Query Match 71.6%; Score 58; DB 2; Length 375;  
Best Local Similarity 71.4%; Pred. No. 0.11;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 KRAAYDQYGHAF 15  
Db 62 KRAAYDQYGHAGVD 75  
||||| :  
RESULT 84  
ID DnaJ\_LACLA STANDARD; PRT; 379 AA.  
AC P35514;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Chaperone protein dnaJ.  
GN Name=dnaJ; OrderedLocusNames=LL2224;  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NIZO RS;  
RX MEDLINE=93194788; PubMed=8449872;  
RA van Asselodonk M., Simons A., Visser H., de Vos W.M., Simons G.;  
RT "Cloning, nucleotide sequence, and regulatory analysis of the  
RT Lactococcus lactis dnaJ gene.";  
RL J. Bacteriol. 175:1637-1644(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IL1403;  
RX MEDLINE=21335186; PubMed=11337471; DOI=10.1101/gr.169701;  
RA Bolotin A., Wincker P., Manger S., Jallou O., Malarne K.,  
RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
RT lactis ssp. lactis IL1403.";

```

RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
DR EMBL; M99413; -; NOT ANNOTATED CDS.
DR EMBL; AE006451; AAK06322.1; -.
DR FIR; A47079; A47079.
DR PIR; H86902; H86902.
DR HSSP; P08622; 1XBL.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; Hsp40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00637; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 5 69 Gly-rich.
FT REPEAT 72 113 CXXCXGKG motif.
FT REPEAT 154 161 CXXCXGKG motif.
FT REPEAT 171 178 CXXCXGKG motif.
FT REPEAT 197 204 CXXCXGKG motif.
FT REPEAT 211 218 CXXCXGKG motif.
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 157 157 Zinc 1 (By similarity).
FT METAL 171 171 Zinc 2 (By similarity).
FT METAL 174 174 Zinc 2 (By similarity).
FT METAL 197 197 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 2 (By similarity).
FT METAL 211 211 Zinc 1 (By similarity).
FT METAL 214 214 Zinc 1 (By similarity).
FT CONFLICT 94 94 G -> S (in Ref. 1).
FT CONFLICT 164 164 A -> R (in Ref. 1).
SQ SEQUENCE 379 AA; 40671 MW; 399CA4EDCB7067B6 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAAYDQYGEA 71

RESULT 85
Q93066 PRELIMINARY; PRT; 379 AA.
AC Q93066;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein DnaJ.

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GN Name=dnaJ;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RA Seerensen K.I., Kilstrup M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AF280940; AAK69493.1; -.
DR HSSP; P08622; 1XBL.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; Hsp40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 40840 MW; 082AFB84DCA6641D CRC64;

Query Match 71.6%; Score 58; DB 2; Length 379;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12
Db 60 QKRAAYDQYGEA 71

RESULT 86
DnaJ CAUCR STANDARD; PRT; 385 AA.
AC P22305;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 46, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
DE Name=dnaJ; OrderedLocusNames=CC0011;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

```



RN	[2]
RP	SEQUENCE OF 1-193 FROM N.A.
RX	MEDLINE=90264295; PubMed=2345134;
RT	Gomes S.L., Gober J.W., Shapiro L.;
RA	"Expression of the Caulobacter heat shock gene dnaK is developmentally
RL	controlled during growth at normal temperatures.";
RL	J. Bacteriol. 172:3051-3059(1990).
CC	-I- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC	the ATPase activity of dnaK (By similarity).
CC	-I- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-I- SIMILARITY: Belongs to the dnaJ family.
CC	-I- SIMILARITY: Contains 1 CR domain.
CC	-I- SIMILARITY: Contains 1 J domain.
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
ENBL	; AE005676; AAK21999.1; --
DR	ENBL; M55224; AAA62724.1; --
PJR	; C87250; C87250.
HSSP	; P08622; 1BQZ.
TIGR	; CC0011; --
InterPro	; IPR002939; DnaJ_C.
InterPro	; IPR001305; DnaJ_CXXCXGKG.
InterPro	; IPR001623; DnaJ_N.
InterPro	; IPR008971; HSP40_DnaJ_pdp.
InterPro	; IPR003095; Hsp_DnaJ.
Pfam	; PF00226; DnaJ; 1.
Pfam	; PF01556; DnaJ_C; 1.
Pfam	; PF00684; DnaJ_CXXCXGKG; 1.
PRINTS	; PR00625; DNAJPROTEIN.
SMART	; SM00271; DnaJ; 1.
PROSITE	; PS00636; DnaJ_1; 1.
PROSITE	; PS00706; DnaJ_2; 1.
PROSITE	; PS00637; DnaJ_CXXCXGKG; 1.
KW	Chaperone; Complete proteome; DNA replication; Heat shock;
KW	Metal-binding; Repeat; Zinc.
FT	DOMAIN 1 70 J-domain.
FT	DOMAIN 77 118 Gly-rich.
FT	REPEAT 148 155 CXXCXGKG motif.
FT	REPEAT 165 172 CXXCXGKG motif.
FT	REPEAT 187 194 CXXCXGKG motif.
FT	REPEAT 201 208 CXXCXGKG motif.
FT	METAL 148 148 Zinc 1 (By similarity).
FT	METAL 151 151 Zinc 1 (By similarity).
FT	METAL 165 165 Zinc 2 (By similarity).
FT	METAL 168 168 Zinc 2 (By similarity).
FT	METAL 187 187 Zinc 2 (By similarity).
FT	METAL 190 190 Zinc 2 (By similarity).
FT	METAL 201 201 Zinc 1 (By similarity).
FT	METAL 204 204 Zinc 1 (By similarity).
FT	CONFLICT 22 23 AF -> RV (in Ref. 2).
FT	CONFLICT 58 58 P -> S (in Ref. 2).
FT	CONFLICT 71 77 GVSGPOG -> AGQRGN (in Ref. 2).
FT	CONFLICT 110 114 RGNSA -> AVOR (in Ref. 2).
FT	CONFLICT 142 147 VPAAMT -> IPRHEP (in Ref. 2).
FT	CONFLICT 161 166 SPVCGV -> QPLCLR (in Ref. 2).
FT	CONFLICT 173 173 R -> P (in Ref. 2).
FT	CONFLICT 185 188 RGCP -> AA (in Ref. 2).
SQ	SEQUENCE 385 AA; 40965 MW; 930181194622B2C5 CRC64;
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	Best Local Similarity 83.3%; Pred. No. 0.11;
	Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	1 QKRAAVDQYGHA 12      ::

RA Calagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
RA Selltreinikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
RA Kothe G.O., Jedd G., Meves W., Staben C., Marcotte E., Greenberg D.,  
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
RA Kamal M., Kamysyellis M., Maucelli E., Bielke C., Rudd S., Frishman D.,  
RA Kryatofova S., Raamussen C., Metzzenberg R.L., Perkins D.D., Kroken S.,  
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,  
RA DeSouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,  
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";  
RL Nature 0:0-0(2003).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data  
DR EMBL; AABX01000451; EAA29179.1; -.  
DR HSSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGXG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pdp.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS50076; DnaJ\_2; 1.  
DR Chapterone; Repeat.  
KW Chapterone; Repeat.  
SQ SEQUENCE 414 AA; 45317 MW; 3A39524BC77567DD CRC64;  
Query Match 71.6%; Score 58; DB 2; Length 414;  
Best Local Similarity 73.3%; Pred. No. 0.12;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 62 QKRAAYDQYGEAGLE 76  
RESULT 89  
Q8LEU4 PRELIMINARY; PRT; 456 AA.  
AC Q8LEU4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein-like.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation.";  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY085227; AAM62460.1; -.  
DR HSSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGXG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pdp.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS50076; DnaJ\_2; 1.  
DR Chapterone; Hypothetical protein; Repeat.  
KW Chapterone; Hypothetical protein; Repeat.  
SQ SEQUENCE 414 AA; 45317 MW; 3A39524BC77567DD CRC64;  
Query Match 71.6%; Score 58; DB 2; Length 414;  
Best Local Similarity 73.3%; Pred. No. 0.12;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 62 QKRAAYDQYGEAGLE 76  
RESULT 89  
Q8LEU4 PRELIMINARY; PRT; 456 AA.  
AC Q8LEU4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DnaJ protein-like.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation.";  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY085227; AAM62460.1; -.  
DR HSSP; P08622; 1BQZ.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
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DR InterPro; IPR001305; DnaJ\_CXXCXGXG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pdp.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ\_1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS50076; DnaJ\_2; 1.  
DR Chapterone; Hypothetical protein; Repeat.  
KW Chapterone; Hypothetical protein; Repeat.  
SQ SEQUENCE 414 AA; 45317 MW; 3A39524BC77567DD CRC64;  
Query Match 71.6%; Score 58; DB 2; Length 456;  
Best Local Similarity 66.7%; Pred. No. 0.13;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 150 EKRDLYDQFGHEAFE 164  
RESULT 90  
Q8NK58 PRELIMINARY; PRT; 188 AA.  
AC Q8NK58;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MDJ1-like protein (Fragment).  
OS Paracoccidioides brasiliensis.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Onygenales; mitosporic Onygenales; Paracoccidioides.  
OX NCBI\_TaxID=121759;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barros T.F., Puccia R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF334811; AAM76975.1; -.  
DR HSSP; P08622; 1EXK.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR001305; DnaJ\_CXXCXGXG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00684; DnaJ\_CXXCXGXG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
KW Repeat.  
FT NON\_TER 1 188  
FT NON\_TER 188 188  
SQ SEQUENCE 188 AA; 19571 MW; A6BF39B944B80C36 CRC64;  
Query Match 70.4%; Score 57; DB 2; Length 188;  
Best Local Similarity 66.7%; Pred. No. 0.08;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QKRAAYDQYGHAAFE 15  
Db 22 EKQAYDRYGAAPD 36  
RESULT 91  
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ID\_DNAJ\_BORBU STANDARD; PRT; 364 AA.  
AC P28616; OS1469;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Chaperone protein dnaJ.  
 GN Name=dnaJ; OrderedLocusNames=BB0517;  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93014224; PubMed=1383161;  
 RA Anzola J., Luft B.J., Gorgone G., Peltz G.;  
 RT "Characterization of a Borrelia burgdorferi dnaJ homolog.";  
 RL Infect. Immun. 60:4965-4968(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93211279; PubMed=8459764;  
 RA Tilly K., Hauser R., Campbell J., Ostheimer G.J.;  
 RT "Isolation of dnaJ, dnaK, and grpE homologues from Borrelia burgdorferi and complementation of Escherichia coli mutants.";  
 RL Mol. Microbiol. 7:359-369(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC 35210 / B31;  
 RA Frazer C.M., Caejens S., Huang W.M., Sutton G.G., Clayton R.A.,  
 RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,  
 RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,  
 RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,  
 RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,  
 RA Gocayne J.D., Weidman J.F., Uterback T.R., Matthey L., McDonald L.A.,  
 RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,  
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;  
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";  
 RL Nature 390:580-586(1997).  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- INDUCTION: By heat shock.  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 CC -1- SIMILARITY: Contains 1 CR domain.  
 CC -1- SIMILARITY: Contains 1 J domain.  
 CC -----  
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 CC -----  
 DR EMBL; M97914; AAA22925.1; -;  
 DR EMBL; M96847; AAA22948.1; -;  
 DR EMBL; AE001154; AAC66888.1; -;  
 DR PIR; D70164; D70164.  
 DR HSSP; P08622; 1BQZ.  
 DR TIGR; BB0517; -;  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
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 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
 DR PRINTS; PR00625; DnaJPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 KW Chaperone; Complete proteome; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.  
 FT DOMAIN 4 69 J-domain.  
 FT DOMAIN 75 87 Gly-rich.

FT REPEAT 148 155 CXXCXGKG motif.  
 FT REPEAT 165 172 CXXCXGKG motif.  
 FT REPEAT 187 194 CXXCXGKG motif.  
 FT REPEAT 201 208 CXXCXGKG motif.  
 FT METAL 148 148 Zinc 1 (By similarity).  
 FT METAL 151 151 Zinc 1 (By similarity).  
 FT METAL 165 165 Zinc 2 (By similarity).  
 FT METAL 168 168 Zinc 2 (By similarity).  
 FT METAL 187 187 Zinc 2 (By similarity).  
 FT METAL 190 190 Zinc 2 (By similarity).  
 FT METAL 201 201 Zinc 1 (By similarity).  
 FT METAL 204 204 Zinc 1 (By similarity).  
 FT CONFLICT 143 143 T -> A (in Ref. 1).  
 FT CONFLICT 296 352 Missing (in Ref. 2).  
 FT CONFLICT 344 352 KLPENLGKE -> NPLKWTAKN (in Ref. 1).  
 SQ SEQUENCE 364 AA; 40498 MW; BE1748AC9BC34082 CRC64;  
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 Best Local Similarity 64.3%; Pred. No. 0.16;  
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KRAAYDOYGHAAPE 15  
 Db 61 KRAAYDRFGHSAPE 74  
 ID Q661A4 PRELIMINARY; PRT; 364 AA.  
 AC Q661A4;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Heat shock protein.  
 GN Name=dnaJ-1; ORFNames=BG0528;  
 OS Borrelia garinii PBI.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 NCBI\_TaxID=290434;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PBI;  
 RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,  
 RA Schulte-Spechtel U., Wilske B., Suehnel J., Platzer M.;  
 RT "Comparative analysis of the Borrelia garinii genome.";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 DR EMBL; CP000013; AAU07167.1; -;  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR GO; GO:0006986; P:response to unfolded protein; IEA.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR InterPro; IPR008162; Pyrophosphatase.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
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 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS00076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
 DR PROSITE; PS00387; PPA5E; UNKNOWN 1.  
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 Query Match 70.4%; Score 57; DB 2; Length 364;  
 Best Local Similarity 64.3%; Pred. No. 0.16;

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Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 2 KKAAYDQYGHAAFE 15
Db 61 KKAAYDQYGHAAFE 74

RESULT 93
Q6Q8U1 PRELIMINARY; PRT; 367 AA.
AC Q6Q8U1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Predicted heat shock protein DnaJ.
GN ORFNames=Red20E09_130;
OS uncultured marine Gamma proteobacterium EBAC20E09.
OC Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;
OC environmental samples.
OX NCBI_TaxID=266134;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15305915;
RA Sabahi G., Beja O., Suzuki M.T., Preston C.M., DeLong E.F.;
RT "Different SAR86 subgroups harbour divergent proteorhodopsins.";
RL Environ. Microbiol. 6:903-910(2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
the ATPase activity of dnaK (By similarity).
CC -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB018706; BAA33936.1; -
CC EMBL; BX321862; CAD85859.1; -
CC HSSP; P08622; 1XBL.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGKG.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR008971; HSP40_DnaJ_pap.
CC InterPro; IPR003095; Hsp_DnaJ.
CC InterPro; IPR011031; Multihem_cyt.
CC Pfam; PF00226; DnaJ_1.
CC Pfam; PF01556; DnaJ_Ci_1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SQ SEQUENCE 367 AA; 40101 MW; FF15AE9B59F7F99F CRC64;

Query Match 70.4%; Score 57; DB 2; Length 367;
Best Local Similarity 60.0%; Pred. No. 0.16;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 QKKAAYDQYGHAAFE 15
Db 61 QKKAAYDQYGHAAFE 75

RESULT 94
DnaJ_NITEU STANDARD; PRT; 369 AA.
AC Q06431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=NE1948;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
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Query Match          70.4%; Score 57; DB 1; Length 369;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGH 12
DB 62 KRAAYDQFGH 72

RESULT 95
ID Q634M8 PRELIMINARY; PRT; 371 AA.
AC Q634M8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chapterone protein.
GN Name=dnaJ; ORFNames=BTZK4060;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16209.1; -.
SQ SEQUENCE 371 AA; 40349 MW; BPDFC56797916010 CRC64;

Query Match          70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 QKRAAYDQYGH 12
DB 60 QKRAAYDQFGH 71

RESULT 96
ID Q6WNG0 PRELIMINARY; PRT; 371 AA.
AC Q6WNG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DnaJ protein.
GN Name=dnaJ; OrderedLocusNames=Bdi1296;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX842649; CAE79192.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.

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DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40776 MW; 00P83F727437C58F CRC64;

Query Match          70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 0.16;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKEAAYDQYGH 14
DB 62 QKRAAYDQFGH 75

RESULT 97
ID Q730M2 PRELIMINARY; PRT; 371 AA.
AC Q730M2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=BCE4394;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AS017278; AAS43295.1; -.
DR TIGR; BCE4394; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.

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SQ SEQUENCE 371 AA; 40363 MW; D9B362A82B670555 CRC64;
Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQVGH 12
    ||||| |||||
Db 60 QKRAAYDQVGH 71

RESULT 98
Q818F0 PRELIMINARY; PRT; 371 AA.
AC Q818F0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN OrderedLocuNames=BC4311;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RN "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AB017012; AAP11224.1; -.
DR HSP; P08622; 1BQZ.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF06684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 371 AA; 40465 MW; 8832D121033F6A27 CRC64;
Query Match 70.4%; Score 57; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQVGH 12
    ||||| |||||
Db 60 QKRAAYDQVGH 71

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RESULT 99
Q81LS3 PRELIMINARY; PRT; 371 AA.
AC Q81LS3; Q6HT78; Q6KMG8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocuNames=BA4538, BAS4212, GBA44538;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rikstad J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RL closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Wavel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AB017038; AAP28247.1; -.
DR EMBL; AB017334; AAT33659.1; -.
DR EMBL; AB017225; AAT56511.1; -.
DR HSP; P08622; 1BQZ.
DR TIGR; BA4538; -.
DR TIGR; GBA44538; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF06684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

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KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 371 AA; 40363 MW; FFD75679791170C CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
Db 60 QKRAQYDQFGHA 71

## RESULT 100

Q6HDK8 PRELIMINARY; PRT; 371 AA.  
AC Q6HDK8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Chaperone protein.  
GN Name=dnaJ; OrderedLocusNames=BT9727.4050;  
OS Bacillus thuringiensis (subsp. konkukian).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=180856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,  
CC the ATPase activity of dnaK (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC EMBL; AE017355; AAT63523.1; -.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR002939; DnaJ\_C.  
DR InterPro; IPR001305; DnaJ\_CXXCXGKG.  
DR InterPro; IPR001623; DnaJ\_N.  
DR InterPro; IPR008971; HSP40\_DnaJ\_dep.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ\_C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXGKG; 1.  
DR PRINTS; PR00625; DnaJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00636; DnaJ\_1; 1.  
DR PROSITE; PS00076; DnaJ\_2; 1.  
DR PROSITE; PS00637; DnaJ\_CXXCXGKG; 1.  
KW Chaperone; Complete proteome; DNA replication; Heat shock;  
KW Metal-binding; Repeat; Zinc.  
SQ SEQUENCE 371 AA; 40363 MW; FFD75679791170C CRC64;

Query Match 70.4%; Score 57; DB 2; Length 371;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGH 12  
Db 60 QKRAQYDQFGHA 71

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